

; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 14
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-11

Query Match 5.0%; Score 32; DB 4; Length 1293;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGGATGGCTGCTGCTG 406
|||||
DB 1146 GTACCCCTGCTGCTGGATGGCTGCTGCTG 1115

RESULT 6
US-09-182-145-117

; Sequence 117, Application US/09182145B
; Patent No. 6387657

; GENERAL INFORMATION:

; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 117
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-51
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-117

Query Match 4.3%; Score 27; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 CCTGTGCTGATGGCTGTGCTGCTG 406
|||||
DB 1 CCTGTGCTGATGGCTGTGCTGCTG 27

RESULT 7
US-09-385-982-220/c

; Sequence 220, Application US/09385982
; Patent No. 6262334

; GENERAL INFORMATION:

; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982

; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(616)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-220

Query Match 3.0%; Score 19; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGCTGGCTTCACC 635
|||||
DB 127 TGATGACGCTGGCTTCACC 109

RESULT 8
US-09-182-145-39

; Sequence 39, Application US/09182145B
; Patent No. 6387657

; GENERAL INFORMATION:

; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 39
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-841
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-39

Query Match 3.0%; Score 19; DB 4; Length 841;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 TGATGCTGTGGCTGCTG 406
|||||
DB 151 TGATGCTGTGGCTGCTG 169

RESULT 9
US-09-149-476-225/C
; Sequence 225, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
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EARLIER APPLICATION NUMBER: 60/043,672
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
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EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
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EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/047,595
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 3.0%; Score 19; DB 4; Length 1220;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 617 TGATGACGGTGCTCACC 635
|||||
Db 128 TGATGACGGTGCTCACC 110

RESULT 11
US-09-213-768-1/c
Sequence 1, Application US/09213768
Patent No. 5985664
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
FILE REFERENCE: RTS-0026
CURRENT APPLICATION NUMBER: US/09/213,768
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1


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; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(441)
US-09-213-768-1
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Query Match          3.0%; Score 19; DB 2; Length 1514;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      617 TGATGACGGTGGCTTCACC 635
      |||||||
Db      136 TGATGACGGTGGCTTCACC 118
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RESULT 12

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US-09-668-680-13
; Sequence 13, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 13
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (130)..(1539)
US-09-668-680-13
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Query Match          3.0%; Score 19; DB 4; Length 1539;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      287 CTTCTCTGCGCTTCTCTCA 305
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Db      774 CTTCTCTGCGCTTCTCTCA 792
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RESULT 13

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US-09-213-768-2/c
; Sequence 2, Application US/09213768
; Patent No. 5985664
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-213-768-2
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Query Match          2.8%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      617 TGATGACGGTGGCTTCAC 634
      |||||||
Db      18 TGATGACGGTGGCTTCAC 1
```

RESULT 14

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US-08-259-451-10
; Sequence 10, Application US/08259451
; Patent No. 6406841
; GENERAL INFORMATION:
; APPLICANT: Lee, Helen H.
; APPLICANT: Swanson, Priscilla A.
; APPLICANT: Idler, Kenneth B.
; APPLICANT: Rosenblatt, Joseph D.
; APPLICANT: Chen, Irvin S. Y.
; APPLICANT: Golde, David W.
; APPLICANT: Robertson, Eugene F.
; APPLICANT: Stephens, John E.
; APPLICANT: Chan, Emerson W.
; APPLICANT: Buytendorp, Mark H.
; APPLICANT: Johnson, Joan E.
; APPLICANT: Motley, Cheryl T.
; APPLICANT: Peterson, Bryan
; APPLICANT: Edwards, Michelle
; APPLICANT: Guidinger, Peggy
; TITLE OF INVENTION: HTLV-IIINRA Compositions
; TITLE OF INVENTION: and Assays for Detecting HTLV Infection
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; MEDIUM TYPE: storage
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,451
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,415
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Daniel W. Collins
; REGISTRATION NUMBER: 31,912
; REFERENCE/DOCKET NUMBER: 5381.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-6365
; TELEFAX: (708) 938-2623
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
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US-08-259-451-10

Query Match 2.8%; Score 18; DB 4; Length 2949;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 193 GGCCTCCACGGCCTCACC 210
|||||
DB 2071 GGCCTCCACGGCCTCACC 2088

RESULT 15

US-08-249-380-1/c
; Sequence 1, Application US/08249380
; Patent No. 5827685

; GENERAL INFORMATION:

APPLICANT: Lindquist, Susan
TITLE OF INVENTION: Methods and Compositions of Genetic
TITLE OF INVENTION: Stress Response Systems
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,380
FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/710,187
FILING DATE: 31-MAY-1991

; ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: ARCD:024

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-787-1400

TELEFAX: 713-789-2679

INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

LENGTH: 3727 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-249-380-1

Query Match

Best Local Similarity 2.8%; Score 18; DB 1; Length 3727;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 ACTGATCCATCTCTGGC 280
|||||
DB 1143 ACTGATCCATCTCTGGC 1126

Search completed: July 28, 2003, 15:58:54
Job time : 35.7003 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:30:21 ; Search time 156.381 Seconds
(without alignments)
8377.033 Million cell updates/sec

Title: US-10-010-408-1_COPY_1_635
Perfect score: 635
Sequence: 1 GACGCTTCGATCTCCAGAG.....GTGATGACGCTGCTTCACC 635

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1439767 seqs, 1031500376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	635	100.0	1708	15	US-10-010-408-1 Sequence 1, Appl1
2	387	60.9	753	15	US-10-010-408-3 Sequence 3, Appl1
3	318	50.1	681	15	US-10-010-408-12 Sequence 12, Appl1
4	210	33.1	210	15	US-10-010-408-8 Sequence 8, Appl1
5	90	14.2	177	15	US-10-010-408-5 Sequence 5, Appl1
6	90	14.2	1734	15	US-10-112-267-17 Sequence 17, Appl1
7	90	14.2	1734	15	US-10-112-267-18 Sequence 18, Appl1
8	32	5.0	738	15	US-10-112-267-38 Sequence 38, Appl1
9	32	5.0	1266	14	US-10-137-866-319 Sequence 319, App
10	32	5.0	1266	14	US-10-146-726-319 Sequence 319, App
11	32	5.0	1266	14	US-10-146-727-319 Sequence 319, App
12	32	5.0	1266	14	US-10-146-788-319 Sequence 319, App
13	32	5.0	1266	14	US-10-152-380-319 Sequence 319, App
14	32	5.0	1266	14	US-10-153-934-319 Sequence 319, App
15	32	5.0	1266	15	US-10-028-072-319 Sequence 319, App
16	32	5.0	1266	15	US-10-121-049-319 Sequence 319, App

17	32	5.0	1266	15	US-10-123-904-319	Sequence 319, App
18	32	5.0	1266	15	US-10-140-470-319	Sequence 319, App
19	32	5.0	1266	15	US-10-175-746-319	Sequence 319, App
20	32	5.0	1266	15	US-10-176-918-319	Sequence 319, App
21	32	5.0	1266	15	US-10-176-921-319	Sequence 319, App
22	32	5.0	1266	15	US-10-137-865-319	Sequence 319, App
23	32	5.0	1266	15	US-10-140-474-319	Sequence 319, App
24	32	5.0	1266	15	US-10-142-431-319	Sequence 319, App
25	32	5.0	1266	15	US-10-143-114-319	Sequence 319, App
26	32	5.0	1266	15	US-10-140-002-319	Sequence 319, App
27	32	5.0	1266	15	US-10-142-419-319	Sequence 319, App
28	32	5.0	1266	15	US-10-123-262-319	Sequence 319, App
29	32	5.0	1266	15	US-10-142-423-319	Sequence 319, App
30	32	5.0	1266	15	US-10-121-050-319	Sequence 319, App
31	32	5.0	1266	15	US-10-141-755-319	Sequence 319, App
32	32	5.0	1266	15	US-10-143-032-319	Sequence 319, App
33	32	5.0	1266	15	US-10-123-108-319	Sequence 319, App
34	32	5.0	1266	15	US-10-123-236-319	Sequence 319, App
35	32	5.0	1266	15	US-10-123-261-319	Sequence 319, App
36	32	5.0	1266	15	US-10-140-921-319	Sequence 319, App
37	32	5.0	1266	15	US-10-140-928-319	Sequence 319, App
38	32	5.0	1266	15	US-10-121-045-319	Sequence 319, App
39	32	5.0	1266	15	US-10-123-292-319	Sequence 319, App
40	32	5.0	1266	15	US-10-123-903-319	Sequence 319, App
41	32	5.0	1266	15	US-10-124-819-319	Sequence 319, App
42	32	5.0	1266	15	US-10-124-822-319	Sequence 319, App
43	32	5.0	1266	15	US-10-140-925-319	Sequence 319, App
44	32	5.0	1266	15	US-10-160-498-319	Sequence 319, App
45	32	5.0	1266	15	US-10-124-824-319	Sequence 319, App

ALIGNMENTS

RESULT 1
US-10-010-408-1
; Sequence 1, Application US/10010408
; Publication No. US20020165185A1
; GENERAL INFORMATION:
; APPLICANT: John J. Castelli, Jr.
; TITLE OF INVENTION: No. US20020165185A1el Heparin-Induced CCN-Like Molecules
; and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,408
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/044,273
; FILING DATE: March 19, 1998
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 1708 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-010-408-1

Query Match 100.0%; Score 635; DB 15; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACGCTTCGATCTCCAGAGGACCCTGGGGTGGGACAGGGCCCTGGCAAGGCTGCAGCC 60
Db 1 GACGCTTCGATCTCCAGAGGACCCTGGGGTGGGACAGGGCCCTGGCAAGGCTGCAGCC 60
OY 61 GCTGGGAGTGGCTTGAATGAGAGTCTTTATTAAGTGAAGTGAAGAGGCTC 120
Db 61 GCTGGGAGTGGCTTGAATGAGAGTCTTTATTAAGTGAAGTGAAGAGGCTC 120
OY 121 CTGTACAGCTTGTCTTAAGTCTTAGCAGTGTGGCTTGGGCTTACACACTGTGAGA 180
Db 121 CTGTACAGCTTGTCTTAAGTCTTAGCAGTGTGGCTTGGGCTTACACACTGTGAGA 180
OY 181 CACCTTCGTGGCTCCACAGGCTCACCTTCAGTTTGAAGTGGCTCCACAGGAG 240
Db 181 CACCTTCGTGGCTCCACAGGCTCACCTTCAGTTTGAAGTGGCTCCACAGGAG 240
OY 241 ACGGTGACATGAGGGGACCCCACTGATCCATCTTCGACCACTTCCCTGCTC 300
Db 241 ACGGTGACATGAGGGGACCCCACTGATCCATCTTCGACCACTTCCCTGCTC 300
OY 301 TCTCAATGTTGTGTGCCAGCTGTGCCGACACCCCTGTACCTGTCTTGACACCA 360
Db 301 TCTCAATGTTGTGTGCCAGCTGTGCCGACACCCCTGTACCTGTCTTGACACCA 360
OY 361 AGTGCCACAGGGGATACCCCTGTGCTGATGAGGCTGTGCTGTAAAGTGTGAC 420
Db 361 AGTGCCACAGGGGATACCCCTGTGCTGATGAGGCTGTGCTGTAAAGTGTGAC 420
OY 421 GGAGGCTGGGAGTCTTCGACCACTGCATGTTCGACACCCAGGAGGCTGTT 480
Db 421 GGAGGCTGGGAGTCTTCGACCACTGCATGTTCGACACCCAGGAGGCTGTT 480
OY 481 GTACAGCTGGGAGGAGGCTGGGAGGAGGCTGCTCTTGATGAGATGACG 540
Db 481 GTACAGCTGGGAGGAGGCTGGGAGGAGGCTGCTCTTGATGAGATGACG 540
OY 541 GTAGCTGTGAGTGAATGGCCGACAGGTACCTGATGAGAGAGCACTTAAACCA 600
Db 541 GTAGCTGTGAGTGAATGGCCGACAGGTACCTGATGAGAGAGCACTTAAACCA 600
OY 601 GGGTCTGTGCGCTGTGATGACGGTGGCTTACC 635
Db 601 GGGTCTGTGCGCTGTGATGACGGTGGCTTACC 635

RESULT 2

US-10-010-408-3
Sequence 3, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 753 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-010-408-3

Query Match 60.9%; Score 387; DB 15; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.6e-194;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 ATGAGGGGACGCCACATGATCCATCTTCGGCCACTTCTCTGCTCTCTCAATG 308
Db 1 ATGAGGGGACGCCACATGATCCATCTTCGGCCACTTCTCTGCTCTCTCAATG 308
OY 309 GTGTGTGCCAGCTGTGCGGACACACCCTGTACCTGTCTTGACACCAAGTCCCA 368
Db 61 GTGTGTGCCAGCTGTGCGGACACACCCTGTACCTGTCTTGACACCAAGTCCCA 368
OY 369 CAGGGGATACCCCTGTGCTGATGGCTGTGCTGTAAAGTGTGACAGGAGGCTG 428
Db 121 CAGGGGATACCCCTGTGCTGATGGCTGTGCTGTAAAGTGTGACAGGAGGCTG 428
OY 429 GGGGAGTCTGCGACCACTGCATGTTCGACACCCAGGAGGCTGTTGTACAGCT 488
Db 181 GGGGAGTCTGCGACCACTGCATGTTCGACACCCAGGAGGCTGTTGTACAGCT 488
OY 489 GGGGAGGCTGCGGAGGAGGAGGCTGTGTCTCTTGATGAGATGAGGAGTACCTGT 548
Db 241 GGGGAGGCTGCGGAGGAGGAGGCTGTGTCTCTTGATGAGATGAGGAGTACCTGT 548
OY 549 GAGGTGAATGCGCGAGTACCTGATGAGAGAGCACTTAAACCAATTCAGAGGCTC 608
Db 301 GAGGTGAATGCGCGAGTACCTGATGAGAGAGCACTTAAACCAATTCAGAGGCTC 608
OY 609 TGCCGCTGTGATGACGGTGGCTTACC 635
Db 361 TGCCGCTGTGATGACGGTGGCTTACC 635

RESULT 3

US-10-010-408-12
Sequence 12, Application US/10010408

Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..681
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-010-408-12

Query Match 50.1%; Score 318; DB 15; Length 681;
Best Local Similarity 100.0%; Pred. No. 7.4e-158;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 CAGCTGTGCGGACACCCCTGTACCTGTCTTGACACACCCAGTGCACAGGGGTA 377
|||||
Db 1 CAGCTGTGCGGACACCCCTGTACCTGTCTTGACACACCCAGTGCACAGGGGTA 60
QY 378 CCCCTGTGCTGATGGCTGTGGCTGCTGTAAAGTGTGTGCACCGAGGCTGGGGAGTCC 437
|||||
Db 61 CCCCTGTGCTGATGGCTGTGGCTGCTGTAAAGTGTGTGCACCGAGGCTGGGGAGTCC 120
QY 438 TGCACACCACTGCATGTCTGCGACCCAGCCAGGGCTGTTGTGCAGCCTGGGGCAGGC 497
|||||
Db 121 TGCACACCACTGCATGTCTGCGACCCAGCCAGGGCTGTTGTGCAGCCTGGGGCAGGC 180
QY 498 CCTGGCGGCCATGGGCTGTGTCTCTTGATGAGGATGACGGTAGCTGTGAGGTGAAT 557
|||||
Db 181 CCTGGCGGCCATGGGCTGTGTCTCTTGATGAGGATGACGGTAGCTGTGAGGTGAAT 240
QY 558 GCGCGCAGGTACCTGGATGAGAGACCTTTAAACCAATTGCAGGGTCTGTGCGGCTGT 617
|||||
Db 241 GCGCGCAGGTACCTGGATGAGAGACCTTTAAACCAATTGCAGGGTCTGTGCGGCTGT 300
QY 618 GATGACGGTGGCTTCACC 635
|||||

Db 301 GATGACGGTGGCTTCACC 318

RESULT 4
US-10-010-408-8
Sequence 8, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..210
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-010-408-8

Query Match 33.1%; Score 210; DB 15; Length 210;
Best Local Similarity 100.0%; Pred. No. 9.4e-101;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 CAGCTGTGCGGACACCCCTGTACCTGTCTTGACACACCCAGTGCACAGGGGTA 377
|||||
Db 1 CAGCTGTGCGGACACCCCTGTACCTGTCTTGACACACCCAGTGCACAGGGGTA 60
QY 378 CCCCTGTGCTGATGGCTGTGGCTGCTGTAAAGTGTGTGCACCGAGGCTGGGGAGTCC 437
|||||
Db 61 CCCCTGTGCTGATGGCTGTGGCTGCTGTAAAGTGTGTGCACCGAGGCTGGGGAGTCC 120
QY 438 TGCACACCACTGCATGTCTGCGACCCAGCCAGGGCTGTTGTGCAGCCTGGGGCAGGC 497
|||||
Db 121 TGCACACCACTGCATGTCTGCGACCCAGCCAGGGCTGTTGTGCAGCCTGGGGCAGGC 180
QY 498 CCTGGCGGCCATGGGCTGTGTCTCTTG 527
|||||
Db 181 CCTGGCGGCCATGGGCTGTGTCTCTTG 210

```
RESULT 5
US-10-010-408-5
; Sequence 5, Application US/10010408
; Publication No. US20020165185A1
; GENERAL INFORMATION:
; APPLICANT: John J. Castellot, Jr.
; TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules
; and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,408
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/044,273
; FILING DATE: March 19, 1998
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..177
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-408-5

Query Match      14.2%; Score 90; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.4e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      546 TGTGAGTGAATGCCGCGAGGTACTGTGATGAGAGACGTTAAACCCCAATTGCAGGGTC 605
Db      1 TGTGAGTGAATGCCGCGAGGTACTGTGATGAGAGACGTTAAACCCCAATTGCAGGGTC 60

OY      606 CTGTGCGCGTGTGATGACGGTGGCTTCACC 635
Db      61 CTGTGCGCGTGTGATGACGGTGGCTTCACC 90

RESULT 6
US-10-112-267-17
; Sequence 17, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 17
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-17

Query Match      14.2%; Score 90; DB 15; Length 1734;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      410 AGTGTGTGACGAGCGCTGGGGAGTCTCGCACCACTGCATGTCTGCGACCCAGCCA 469
Db      418 AGTGTGTGACGAGCGCTGGGGAGTCTCGCACCACTGCATGTCTGCGACCCAGCCA 477

OY      470 GGGCCTGTTTGTCTCAGCCTGGGGCAGGCC 499
Db      478 GGGCCTGTTTGTCTCAGCCTGGGGCAGGCC 507

RESULT 7
US-10-112-267-18/c
; Sequence 18, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 18
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-18

Query Match      14.2%; Score 90; DB 15; Length 1734;
```

```
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTCACGAGGCTGGGGAGTCTCGCAGCACCCTGCATGTCTCGACCCAGCCA 469
DB 1317 AGTGTGTCACGAGGCTGGGGAGTCTCGCAGCACCCTGCATGTCTCGACCCAGCCA 1258

QY 470 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 499
DB 1257 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 1228

RESULT 8
US-10-112-267-38
; Sequence 38, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 38
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-267-38

Query Match 5.0%; Score 32; DB 15; Length 738;
Best Local Similarity 100.0%; Pred. No. 9.6e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGATGGCTGTGCTGCTG 406
DB 115 GTACCCCTGTGCTGATGGCTGTGCTGCTG 146

RESULT 9
US-10-137-866-319
; Sequence 319, Application US/10137866
; Publication No. US20030129689A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C151
; CURRENT APPLICATION NUMBER: US/10/137,866
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
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;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/066453
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/066511
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/069212
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/069278
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/069334
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/069694
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 60/072320
;; PRIOR FILING DATE: 1998-01-23
;; PRIOR APPLICATION NUMBER: 60/073612
;; PRIOR FILING DATE: 1998-02-04
;; PRIOR APPLICATION NUMBER: 60/074086
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/074092
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-02-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081695
;; PRIOR FILING DATE: 1998-04-14
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081818
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082999
;; PRIOR FILING DATE: 1998-04-24
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085149
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086414

;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/086430
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088730
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088741
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982

Query Match 5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGCGCTG 406
|||||
Db 136 GTACCCCTGCTGCTGATGCGCTGTGCGCTG 167

RESULT 10
US-10-146-726-319
; Sequence 319, Application US/10146726
; Publication No. US20030129690A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin J.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C308


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; CURRENT APPLICATION NUMBER: US/10/146,726
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-726-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 406
    |||
Db 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

RESULT 11
US-10-146-727-319
; Sequence 319, Application US/10146727
; Publication No. US20030129691A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C312
; CURRENT APPLICATION NUMBER: US/10/146,727
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-727-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 406
    |||
Db 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

RESULT 12
US-10-146-788-319
; Sequence 319, Application US/10146788
; Publication No. US20030129693A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

```
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C322
; CURRENT APPLICATION NUMBER: US/10/146,788
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-146-788-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 406
    |||
Db 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

RESULT 13
US-10-152-380-319
; Sequence 319, Application US/10152380
; Publication No. US20030129694A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C397
; CURRENT APPLICATION NUMBER: US/10/152,380
; CURRENT FILING DATE: 2002-05-21
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-152-380-319

Query Match          5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 375 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 406
|||||
Db 136 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 167

RESULT 14

US-10-153-934-319
; Sequence 319, Application US/10153934
; Publication No. US20030129695A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C412
; CURRENT APPLICATION NUMBER: US/10/153,934
; CURRENT FILING DATE: 2002-05-22
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-153-934-319

Query Match 5.0%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 406
|||||
Db 136 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 167

RESULT 15

US-10-028-072-319
; Sequence 319, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
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; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 5.0%; Score 32; DB 15; Length 1266;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY . 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 136 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 167

Search completed: July 28, 2003, 15:36:32
Job time : 157.381 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:16:26 ; Search time 1126.46 Seconds
(without alignments)
9129.604 Million cell updates/sec

Title: US-10-010-408-1_COPY_1_635
Perfect score: 635
Sequence: 1 GACGCTTCTGATCTCCAGAG.....GTGATGACGGTGGCTTCACC.635

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inu:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	14.2	940	14	BQ937887
2	67	10.6	537	14	BQ560868
3	49	7.7	424	10	BB849097
4	32	5.0	380	12	BG900020
5	32	5.0	405	12	BG900069
6	32	5.0	618	12	BG538695

7	32	5.0	620	13	BG928868	BG928868	HNC57-1-D
8	32	5.0	651	13	BI457141	BI457141	603185392
9	32	5.0	749	9	AL555144	AL555144	603185392
10	32	5.0	750	13	BM043988	BM043988	603620978
11	32	5.0	800	13	BI826781	BI826781	603077268
12	32	5.0	886	13	BI822142	BI822142	603039845
13	32	5.0	888	13	BI825652	BI825652	603072631
14	32	5.0	916	13	BI457367	BI457367	603185689
15	32	5.0	928	13	BI161474	BI161474	602864871
16	32	5.0	933	14	BQ278961	BQ278961	AGENCOURT
17	32	5.0	979	14	BQ279131	BQ279131	AGENCOURT
18	32	5.0	1006	14	BM921531	BM921531	AGENCOURT
19	32	5.0	1058	14	BM805088	BM805088	AGENCOURT
20	32	5.0	1073	14	BQ073722	BQ073722	AGENCOURT
21	32	5.0	1166	13	BM543799	BM543799	AGENCOURT
22	32	5.0	1251	14	BQ961357	BQ961357	AGENCOURT
23	30	4.7	190	9	AA647775	AA647775	vp04c09.r
24	23	3.6	436	17	AQ095651	AQ095651	HS_3017_A
25	23	3.6	742	13	BI758148	BI758148	603023866
26	23	3.6	792	13	BI823598	BI823598	603040962
27	21	3.3	495	13	BI204749	BI204749	EST522789
28	21	3.3	529	9	AI897896	AI897896	EST267339
29	21	3.3	561	12	BF051668	BF051668	EST436915
30	21	3.3	563	9	AI897344	AI897344	EST266787
31	21	3.3	609	9	AI485142	AI485142	EST243446
32	21	3.3	620	10	AW223381	AW223381	EST300192
33	20	3.1	232	9	AL658941	AL658941	AL658941
34	20	3.1	251	9	AI303895	AI303895	u162f11.y
35	20	3.1	288	10	BE574058	BE574058	IPBrn0148
36	20	3.1	332	17	AZ650040	AZ650040	1M0520D04
37	20	3.1	381	10	BE537338	BE537338	601064521
38	20	3.1	391	9	AI147346	AI147346	qg63h04.s
39	20	3.1	452	10	BE481184	BE481184	166529.BA
40	20	3.1	475	9	AA862947	AA862947	og98d01.s
41	20	3.1	485	9	AA862518	AA862518	oh06e04.s
42	20	3.1	488	9	AA630630	AA630630	ac11f11.s
43	20	3.1	489	9	AA878562	AA878562	oj17a12.s
44	20	3.1	509	9	AI002710	AI002710	an20d07.s
45	20	3.1	512	9	AA443583	AA443583	zw35a09.s

ALIGNMENTS

RESULT 1
BQ937887 940 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 8951807 NCI_CGAP_C024 Mus musculus cDNA clone
DEFINITION IMAGE:6476852 5', mRNA sequence.
ACCESSION BQ937887
VERSION BQ937887.1 GI:22353365
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAMA14017 row: n column: 21
High quality sequence stop: 543.
Location/Qualifiers
1..940

FEATURES
source

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6476852"
/clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT;
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 169 a 277 c 288 g 200 t 6 others
ORIGIN

Query Match 14.2%; Score 90; DB 14; Length 940;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTGACGAGGCTGGGGAGTCTGCAGCACCCTGCATGTCTGCAGCCAGCCA 469
|||||
DB 444 AGTGTGTGACGAGGCTGGGGAGTCTGCAGCACCCTGCATGTCTGCAGCCAGCCA 503

OY 470 GGGCCTGTTGTACGCTGGGGCAGGCC 499
|||||
DB 504 GGGCCTGTTGTACGCTGGGGCAGGCC 533

RESULT 2
BO560868 537 bp mRNA linear EST 20-JUN-2002
LOCUS H4067A01-5 NIA Mouse 7.4K CDNA Clone Set Mus musculus cDNA clone
DEFINITION H4067A01 5', mRNA sequence.
ACCESSION BO560868
VERSION BO560868.1 GI:21461753
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 537)
AUTHORS Vanburen,V., Plao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin
P.R., Stagg,C.A., Bassey,U., Aliba,K., Hamatani,T., Kargul,G.J.,
Luo,A.G. and Ko,M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL Unpublished (2002)
COMMENT Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdaelgusun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4067 row: A column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 537
POLYA=No.

FEATURES
source Location/Qualifiers

1..537
/organism="Mus musculus"

/strain="C57BL/6"

/db_xref="niaEST:H4067A01-5"

/db_xref="taxon:10090"

/clone="H4067A01"

/clone_lib="NIA Mouse 7.4K CDNA Clone Set"

/sex="mixed"

/dev_stage="mixed"

/lab_host="DH10B"

/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

BASE COUNT 87 a 162 c 166 g 122 t
ORIGIN

Query Match 10.6%; Score 67; DB 14; Length 537;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTGACGAGGCTGGGGAGTCTGCAGCACCCTGCATGTCTGCAGCCAGCCA 469
|||||
DB 471 AGTGTGTGACGAGGCTGGGGAGTCTGCAGCACCCTGCATGTCTGCAGCCAGCCA 530

OY 470 GGGCCTG 476
|||||
DB 531 GGGCCTG 537

RESULT 3
BB849097 424 bp mRNA linear EST 26-NOV-2001
LOCUS BB849097
DEFINITION BB849097 RIKEN full-length enriched, adult inner ear Mus musculus
cDNA clone F930006G02 5', mRNA sequence..
ACCESSION BB849097
VERSION BB849097.1 GI:17090551
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 424)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)

JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10
(11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
source Location/Qualifiers

1..424

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="F930006G02"

/clone_lib="RIKEN full-length enriched, adult inner ear"

/tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues ; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"

BASE COUNT 65 a 124 c 132 g 103 t
ORIGIN

Query Match 7.7%; Score 49; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGCACGAGGCTGGGGAGTCTCGCACCACTGCATGCTGC 458
|||||
Db 373 AGTGTGTGCACGAGGCTGGGGAGTCTCGCACCACTGCATGCTGC 421

RESULT 4
BG900020 380 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA48-1-G2.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA
, mRNA sequence.
ACCESSION BG900020
VERSION BG900020.1 GI:14310269
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 380)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 58 a 139 c 118 g 65 t
ORIGIN

Query Match 5.0%; Score 32; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 406
|||||
Db 206 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 237

RESULT 5
BG900069

LOCUS BG900069 405 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA51-1-A11.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
cDNA, mRNA sequence.
ACCESSION BG900069
VERSION BG900069.1 GI:14310318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 62 a 140 c 135 g 68 t
ORIGIN

Query Match 5.0%; Score 32; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 406
|||||
Db 202 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 233

RESULT 6
BG538695 618 bp mRNA linear EST 03-APR-2001
DEFINITION 602566932F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691574 5',
mRNA sequence.
ACCESSION BG538695
VERSION BG538695.1 GI:13530928
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLCM1510 row: p column: 07
High quality sequence stop: 499.

FEATURES

source

Location/Qualifiers
1. .618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4691574"
/clone_1lb="NIH_MGC_77"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcggcc); Site_2: SfiI (ggccatattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATCTAGAGGCCGAGGGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T); Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT
ORIGIN

95 a 194 c 213 g 116 t

Query Match 5.0%; Score 32; DB 12; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

375 GTACCCCTGTGCTGATGCTGTGGCTGCTG 406
|||||

Db

291 GTACCCCTGTGCTGATGCTGTGGCTGCTG 322

RESULT 7
LOCUS

620 bp mRNA linear EST 06-NOV-2001
HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 620)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.

TITLE

Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries

JOURNAL
MEDLINE

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

COMMENT

Contact: Sanjay Kumar
UW2109

GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com

FEATURES

source

Seq primer: T7.

Location/Qualifiers
1. .620
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="HNC (Human Normal Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
directional"

BASE COUNT
ORIGIN

97 a 218 c 207 g 98 t

Query Match 5.0%; Score 32; DB 13; Length 620;

Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

375 GTACCCCTGTGCTGATGCTGTGGCTGCTG 406
|||||

Db

210 GTACCCCTGTGCTGATGCTGTGGCTGCTG 241

RESULT 8
LOCUS

651 bp mRNA linear EST 21-AUG-2001
BI457141
603185392F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258159 5',
mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 651)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1869 row: g column: 24
High quality sequence stop: 651.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1. .651
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258159"
/clone_1lb="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. I"

BASE COUNT
ORIGIN

91 a 230 c 219 g 111 t

Query Match 5.0%; Score 32; DB 13; Length 651;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

375 GTACCCCTGTGCTGATGCTGTGGCTGCTG 406
|||||

Db

96 GTACCCCTGTGCTGATGCTGTGGCTGCTG 127

RESULT 9
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

749 bp mRNA linear EST 16-FEB-2001
AL555144 LTI_NFL006_PU2 Homo sapiens cDNA clone CS0DK007YO21 5
prime, mRNA sequence.

AL555144

AL555144

AL555144.1 GI:12896595

EST.

human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 749)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de-Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 749
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODK007Y021"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 128 a 252 c 236 g 133 t

ORIGIN

Query Match 5.0%; Score 32; DB 9; Length 749;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 406
|||||
Db 432 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 463

RESULT 10 750 bp mRNA linear EST 07-NOV-2001
BM043988 603620978F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5446794 5',
LOCUS mRNA sequence.
DEFINITION
ACCESSION BM043988
VERSION BM043988.1 GI:16773255
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 750)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1929 row: k column: 19
High quality sequence stop: 714.
Location/Qualifiers
1. 750
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5446794"
/clone_lib="NIH_MGC_40"

/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 112 a 267 c 246 g 125 t

ORIGIN

Query Match 5.0%; Score 32; DB 13; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 406
|||||
Db 142 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 173

RESULT 11 800 bp mRNA linear EST 04-OCT-2001
BI826781 603077268F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5169065 5',
LOCUS mRNA sequence.
DEFINITION
ACCESSION BI826781
VERSION BI826781.1 GI:15938331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11420 row: g column: 18
High quality sequence stop: 788.
Location/Qualifiers
1. 800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5169065"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

BASE COUNT 115 a 284 c 264 g 136 t 1 others

ORIGIN

Query Match 5.0%; Score 32; DB 13; Length 800;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 120 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 151

RESULT 12
BI822142 886 bp mRNA linear EST 04-OCT-2001
LOCUS 603039845F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180650 5',
DEFINITION mRNA sequence.
ACCESSION BI822142
VERSION BI822142.1 GI:15933692
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11450 row: j column: 11
High quality sequence stop: 865.

FEATURES
source
1. 886
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5180650"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1. male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 134 a 310 c 288 g 154 t

ORIGIN

Query Match 5.0%; Score 32; DB 13; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 121 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 152

RESULT 13
BI825652 888 bp mRNA linear EST 04-OCT-2001
LOCUS 603072631F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164614 5',
DEFINITION mRNA sequence.
ACCESSION BI825652
VERSION BI825652.1 GI:15937202
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 888)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11408 row: n column: 07
High quality sequence stop: 877.

FEATURES
source
1. 888
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5164614"
/clone_11b="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

BASE COUNT 130 a 308 c 288 g 162 t

ORIGIN

Query Match 5.0%; Score 32; DB 13; Length 888;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 117 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 148

RESULT 14
BI457367 916 bp mRNA linear EST 21-AUG-2001
LOCUS 603185689F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258398 5',
DEFINITION mRNA sequence.
ACCESSION BI457367
VERSION BI457367.1 GI:15248023
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 916)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1870 row: a column: 23
High quality sequence stop: 778.

FEATURES
source
1. 916
location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258398"
/clone_1b="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-DBT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

```

Query Match	5.08;	Score 32;	DB 13;	Length 916;
Best Local Similarity	100.0%;	Pred. No. 0.00017;		
Matches	32;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;
Oy	375	GTACCCCTGGTGGCTGATGCTGTGCTG	406	
Db	96	GTACCCCTGGTGGCTGATGCTGTGCTG	127	

RESULT 15	
BI161474	
LOCUS	BI161474
DEFINITION	602864871.F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5019065 5', mRNA sequence.

ACCESSION	BI161474	
VERSION	BI161474.1	GI:14621475
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens	1 (bases 1 to 928)	NIH-MGC	http://mgc.ncl.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLCM1833 row: m column: 18
High quality sequence start: 28
High quality sequence stop: 756.

FEATURES	location/Qualifiers
source	1. .928

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="IMAGE:5019065"
/clone_1b="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

```

ORIGIN		Query Match	Best Local Similarity	Score 32;	DB 13;	Length 928;
Matches	32;	Conservative	0;	Mismatches	0;	Gaps 0;
QY	375	GTACCCCTGGTGCCTGCGATGCGCTGTGGCTGCTG	406			
Db	188	GTACCCCTGGTGCCTGCGATGCGCTGTGGCTGCTG	219			

Search completed: July 28, 2003, 18:02:05
Job time : 1127.46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:19:16 ; Search time 2453.86 Seconds
(without alignments)
10472.371 Million cell updates/sec

Title: US-10-010-408-1_COPY_1_883
Perfect score: 883
Sequence: 1 GACGCTTCTGATCTCCAGAG.....ACCACCTGTGGCTGGCAT 883

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	218	24.7	137964	2	AC126895	AC126895 Rattus no
2	218	24.7	226303	2	AC095418	AC095418 Rattus no
3	166	18.8	137964	2	AC126895	AC126895 Rattus no
4	117	13.3	1741	10	AF259981	AF259981 Rattus no
5	90	10.2	1734	6	AR210324	AR210324 Sequence
6	90	10.2	1734	6	AR210325	AR210325 Sequence
7	90	10.2	1734	10	AF100778	AF100778 Mus muscu
8	90	10.2	61072	10	AL731698	AL731698 Mouse DNA
9	90	10.2	216757	2	AL669906	AL669906 Mus muscu
10	80	9.1	1739	10	AF126063	AF126063 Mus muscu
11	32	3.6	738	6	AR210337	AR210337 Sequence
12	32	3.6	841	6	AR210338	AR210338 Sequence
13	32	3.6	1266	6	AX076919	AX076919 Sequence
14	32	3.6	1266	6	AX464186	AX464186 Sequence
15	32	3.6	1283	9	AF083500	AF083500 Homo sapi
16	32	3.6	1293	6	AR210322	AR210322 Sequence
17	32	3.6	1293	6	AR210323	AR210323 Sequence
18	32	3.6	1309	9	AF074604	AF074604 Homo sapi
19	32	3.6	1427	9	AF100780	AF100780 Homo sapi
20	32	3.6	1450	9	BC017782	BC017782 Homo sapi
21	32	3.6	107260	9	AL139352	AL139352 Human DNA
22	27	3.1	51	6	AR210371	AR210371 Sequence
23	27	3.1	51	6	AX076923	AX076923 Sequence
24	22	2.5	99395	2	AC010446	AC010446 Homo sapi
25	22	2.5	142142	2	AC091173	AC091173 Homo sapi
26	22	2.5	149483	2	AC110904	AC110904 Mus muscu
27	22	2.5	180464	2	AC116351	AC116351 Homo sapi
28	22	2.5	186676	9	AC067881	AC067881 Homo sapi
29	22	2.5	200050	1	AL646068	AL646068 Ralstonia
30	21	2.4	66908	2	AC119914	AC119914 Mus muscu
31	21	2.4	150944	2	AC112856	AC112856 Rattus no
32	21	2.4	154881	2	AC122102	AC122102 Rattus no
33	21	2.4	181343	10	AL671882	AL671882 Mouse DNA
34	21	2.4	204937	2	AL831741	AL831741 Mus muscu
35	21	2.4	215105	2	AC073717	AC073717 Mus muscu
36	20	2.3	1003	5	CHKTCEAA	M73064 Chicken T-C
37	20	2.3	1200	6	AX122384	AX122384 Sequence
38	20	2.3	1221	9	HSM801506	AL133637 Homo sapi
39	20	2.3	1481	8	AB033535	AB033535 Oryza sat
40	20	2.3	3301	9	BC019257	BC019257 Homo sapi
41	20	2.3	4467	9	AB020659	AB020659 Homo sapi
42	20	2.3	7172	10	AB008516	AB008516 Mus muscu
43	20	2.3	36296	9	HSE81G9	282180 Human DNA s
44	20	2.3	83021	2	AC095541	AC095541 Rattus no
45	20	2.3	84001	9	AL162739	AL162739 Human DNA

ALIGNMENTS

RESULT 1
AC126895 137964 bp DNA linear HTG 24-JUL-2002
LOCUS
DEFINITION
Rattus norvegicus clone CH230-301E4, *** SEQUENCING IN PROGRESS
***, 49 unordered pieces.
ACCESSION
AC126895
VERSION
AC126895.1 GI:21724040
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
Rattus norvegicus.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 137964)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowle,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
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Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtonson,J., Newtonson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
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Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
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Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 137964)
Worley,K.C.

Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 137964)
Worley,K.C.

Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One.
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZHG
Center clone name: CH230-301E4
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 89474 bases at least Q40
Consensus quality: 93422 bases at least Q30
Consensus quality: 96506 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 49 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

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1057 1056: contig of 1056 bp in length
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2436 2435: gap of unknown length
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3543 3542: gap of unknown length
5082 5081: contig of 1539 bp in length
5182 5181: gap of unknown length
6425 6424: contig of 1243 bp in length
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9254 9253: gap of unknown length
9254 10445: contig of 1192 bp in length
10446 10445: gap of unknown length
10546 11771: contig of 1226 bp in length
11772 11871: gap of unknown length
11872 13240: contig of 1369 bp in length
13241 13340: gap of unknown length
13341 14359: contig of 1019 bp in length
14360 14459: gap of unknown length
14460 15651: contig of 1192 bp in length
15652 15751: gap of unknown length
15752 17494: contig of 1743 bp in length
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17595 18679: contig of 1085 bp in length
18780 18779: gap of unknown length
18780 20681: contig of 1902 bp in length
20682 20781: gap of unknown length
20782 22118: contig of 1337 bp in length
22119 22218: gap of unknown length
22219 23578: contig of 1360 bp in length
23579 23678: gap of unknown length
23679 25423: contig of 1745 bp in length
25424 25523: gap of unknown length
25524 27808: contig of 2285 bp in length
27809 27908: gap of unknown length
27909 30272: contig of 2364 bp in length
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30373 33091: contig of 2719 bp in length
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33192 35777: contig of 2586 bp in length
35778 35877: gap of unknown length
35879 36908: contig of 1031 bp in length
36909 37008: gap of unknown length
37009 38930: contig of 1922 bp in length
38931 39030: gap of unknown length
39031 41210: contig of 2180 bp in length
41211 41310: gap of unknown length
41311 42937: contig of 1627 bp in length
42938 43037: gap of unknown length
43038 46120: contig of 3083 bp in length
46121 46220: gap of unknown length
46221 48217: contig of 1997 bp in length
48218 48317: gap of unknown length
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50534 52880: contig of 2347 bp in length
52881 55194: gap of unknown length
52981 55194: contig of 2214 bp in length
55195 55294: gap of unknown length
55295 57482: contig of 2188 bp in length
57483 57582: gap of unknown length
57583 60781: contig of 3199 bp in length
60782 60881: gap of unknown length
60882 62599: contig of 1718 bp in length

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* 62600 62699: gap of unknown length
* 62700 65203: contig of 2504 bp in length
* 65204 65303: gap of unknown length
* 65304 66914: contig of 1611 bp in length
* 66915 67014: gap of unknown length
* 67015 70839: contig of 3825 bp in length
* 70840 70939: gap of unknown length
* 70940 75139: contig of 4200 bp in length
* 75140 75239: gap of unknown length
* 75240 78296: contig of 3057 bp in length
* 78297 78396: gap of unknown length
* 78397 83138: contig of 4742 bp in length
* 83139 83238: gap of unknown length
* 83239 88204: contig of 4966 bp in length
* 88205 88304: gap of unknown length
* 88305 92238: contig of 3934 bp in length
* 92239 92338: gap of unknown length
* 92339 97339: contig of 5001 bp in length
* 97340 97439: gap of unknown length
* 97440 103534: contig of 6095 bp in length
* 103535 103634: gap of unknown length
* 103635 107080: contig of 3446 bp in length
* 107081 107180: gap of unknown length
* 107181 115201: contig of 8021 bp in length
* 115202 115301: gap of unknown length
* 115302 121237: contig of 5936 bp in length
* 121238 121337: gap of unknown length
* 121338 127910: contig of 6573 bp in length
* 127911 128010: gap of unknown length
* 128011 137964: contig of 9954 bp in length.
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FEATURES
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    1. .137964
      /organism="Rattus norvegicus"
      /db_xref="taxon:10116"
      /clone="CH230-301E4"
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BASE COUNT 31831 a 34027 c 35229 g 31979 t 4898 others
ORIGIN
```

```
Query Match 24.7%; Score 218; DB 2; Length 137964;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 308 GGTGTGTGCCAGCTGTGCGGACACCCCTGTACTGTTCCTTGACACACCCCACTGCCC 367
      |||||||
DB 104664 GGTGTGTGCCAGCTGTGCGGACACCCCTGTACTGTTCCTTGACACACCCCACTGCCC 104723

QY 368 ACAGGGGTACCCCTGTGCTGATGCGCTGTGGCTGCTGTAAGTGTGTGACGAGGCT 427
      |||||||
DB 104724 ACAGGGGTACCCCTGTGCTGATGCGCTGTGGCTGCTGTAAGTGTGTGACGAGGCT 104783

QY 428 GGGGAGTCTCTGCGACCACTGCATGCTGCGACCCCAAGCCAGGGCCTGTTTGTACGCC 487
      |||||||
DB 104784 GGGGAGTCTCTGCGACCACTGCATGCTGCGACCCCAAGCCAGGGCCTGTTTGTACGCC 104843

QY 488 TGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTCTCT 525
      |||||||
DB 104844 TGGGGCAGGCCCTGGCGGCCATGGGGCTGTGTCTCT 104881
```

```
RESULT 2
LOCUS AC095418 226303 bp DNA linear HTG 11-JUL-2002
DEFINITION Rattus norvegicus clone CH230-7C10, *** SEQUENCING IN PROGRESS ***,
51 unordered pieces.
ACCESSION AC095418
VERSION AC095418.3 GI:21717893
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
```

```
REFERENCE 1 (bases 1 to 226303)
```

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J., Benton,J., Bimarge,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Coyle,M.D., Dathorne,S.R., David,R., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Hollway,C., Hollins,B., Homsl,F., Howard,S., Huber,J., Hulik,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louised,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vlnson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

TITLE

JOURNAL
REFERENCE
2 (bases 1 to 226303)

AUTHORS

JOURNAL

REFERENCE

JOURNAL

TITTLE

JOURNAL

COMMENT

JOURNAL

Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17941885.

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-helpebcm.tmc.edu

Center Project name: GCDF

Center clone name: CH230-7C10

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 185950 bases at least Q40

Consensus quality: 190362 bases at least Q30

Consensus quality: 193076 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 51 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1051: contig of 1051 bp in length
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* 1152 2286: contig of 1135 bp in length
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* 2387 3433: contig of 1047 bp in length
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* 7874 9530: contig of 1657 bp in length
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* 10762 11958: contig of 1197 bp in length
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* 14878 16063: contig of 1186 bp in length
* 16064 16163: gap of unknown length
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* 17586 17686: gap of unknown length
* 17686 18916: contig of 1231 bp in length
* 18917 19016: gap of unknown length
* 19017 20305: contig of 1289 bp in length
* 20306 20405: gap of unknown length
* 20406 21537: contig of 1132 bp in length
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* 21638 23703: contig of 2066 bp in length
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* 23804 26306: contig of 2503 bp in length
* 26307 26406: gap of unknown length
* 26407 28431: contig of 2025 bp in length
* 28432 28531: gap of unknown length
* 28532 30615: contig of 2084 bp in length
* 30616 30715: gap of unknown length
* 30716 33215: contig of 2500 bp in length
* 33216 33315: gap of unknown length
* 33316 35357: contig of 2042 bp in length
* 35358 35458: gap of unknown length
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* 38113 40338: contig of 2226 bp in length
* 40339 40438: gap of unknown length
* 40439 44051: contig of 3613 bp in length
* 44052 44151: gap of unknown length
* 44152 46294: contig of 2143 bp in length
* 46295 46394: gap of unknown length
* 46395 48845: contig of 2451 bp in length
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* 119939 126340: gap of unknown length
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* 149819 149918: gap of unknown length
* 149919 158719: contig of 8801 bp in length
* 158720 158819: gap of unknown length
* 158820 169868: contig of 11049 bp in length
* 169869 169968: gap of unknown length
* 169969 180390: contig of 10422 bp in length
* 180391 180491: gap of unknown length
* 180491 191272: contig of 10782 bp in length
* 191273 191372: gap of unknown length
* 191373 209667: contig of 18295 bp in length
* 209668 209767: gap of unknown length
* 209768 226303: contig of 16536 bp in length.

FEATURES
source 1. .226303
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-7C10"

BASE COUNT 57875 a 53353 c 52917 g 57041 t 5117 others

Query Match 24.7%; Score 218; DB 2; Length 226303;
Best Local Similarity 100.0%; Pred. No. 1.9e-105;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 GGTGTGTGCCAGCTGTGCCGACACCCCTGTACTGTCTTGACACACCCCAAGTCCC 367
|||||
Db 147645 GGTGTGTGCCAGCTGTGCCGACACCCCTGTACTGTCTTGACACACCCCAAGTCCC 147704

QY 368 ACAGGGGGTACCCCTGTGCTGATGGCTGTGGCTGTAAAGTGTGACGAGGCT 427
|||||
Db 147705 ACAGGGGGTACCCCTGTGCTGATGGCTGTAAAGTGTGACGAGGCT 147764

QY 428 GGGGAGTCTTGCACACCTGCATGTTCGACCCAGCGGCTGTTGTCAGCC 487
|||||
Db 147765 GGGGAGTCTTGCACACCTGCATGTTCGACCCAGCGGCTGTTGTCAGCC 147824

QY 488 TGGGGCAGGCCCTGGCGCCATGGGCTGTGTCTCT 525
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Db 147825 TGGGGCAGGCCCTGGCGCCATGGGCTGTGTCTCT 147862

RESULT 3
AC126895/c 137964 bp DNA linear HTG 24-JUL-2002
LOCUS Rattus norvegicus clone CH230-301E4, *** SEQUENCING IN PROGRESS
DEFINITION *** 49 unordered pieces.
ACCESSION AC126895
VERSION AC126895.1 GI:21724040
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Rattus norvegicus.

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 137964)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Newton,N., Nguyen,A., Nguyen,S.,
Moser,M., Neal,D., Newton,J., Newson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oyiedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 137964)
Worley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>.
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZHG
Center clone name: CH230-301E4
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 89474 bases at least Q40
Consensus quality: 93422 bases at least Q30

Consensus quality: 96506 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 49 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1057 1056: contig of 1056 bp in length
* 1157 1156: gap of unknown length
* 2335 2335: contig of 1179 bp in length
* 2336 2435: gap of unknown length
* 2436 3442: contig of 1007 bp in length
* 3443 3542: gap of unknown length
* 3543 5081: contig of 1539 bp in length
* 5082 5181: gap of unknown length
* 5081 6424: contig of 1243 bp in length
* 5182 6524: gap of unknown length
* 6425 7814: contig of 1290 bp in length
* 7815 7914: gap of unknown length
* 7915 9153: contig of 1239 bp in length
* 9154 9253: gap of unknown length
* 9254 10445: contig of 1192 bp in length
* 10446 10545: gap of unknown length
* 10546 11771: contig of 1226 bp in length
* 11772 11771: gap of unknown length
* 11872 13240: contig of 1369 bp in length
* 13241 13340: gap of unknown length
* 13341 14359: contig of 1019 bp in length
* 14360 14459: gap of unknown length
* 14460 15651: contig of 1192 bp in length
* 15652 15751: gap of unknown length
* 15752 17494: contig of 1743 bp in length
* 17495 17594: gap of unknown length
* 17595 18679: contig of 1085 bp in length
* 18680 18779: gap of unknown length
* 18780 20681: contig of 1902 bp in length
* 20682 20781: gap of unknown length
* 20782 22118: contig of 1337 bp in length
* 22119 22218: gap of unknown length
* 22219 23578: contig of 1360 bp in length
* 23579 23678: gap of unknown length
* 23679 25423: contig of 1745 bp in length
* 25424 25523: gap of unknown length
* 25524 27808: contig of 2285 bp in length
* 27809 27908: gap of unknown length
* 27909 30272: contig of 2364 bp in length
* 30273 30372: gap of unknown length
* 30373 33091: contig of 2719 bp in length
* 33092 33191: gap of unknown length
* 33192 35777: contig of 2586 bp in length
* 35778 35877: gap of unknown length
* 35878 36908: contig of 1031 bp in length
* 36909 37008: gap of unknown length
* 37009 38930: contig of 1922 bp in length
* 38931 39030: gap of unknown length
* 39031 41210: contig of 2180 bp in length
* 41211 41310: gap of unknown length
* 41311 42937: contig of 1627 bp in length
* 42938 43037: gap of unknown length
* 43038 46120: contig of 3083 bp in length
* 46121 46220: gap of unknown length
* 46221 48317: contig of 1997 bp in length
* 48218 48317: gap of unknown length
* 48318 50433: contig of 2116 bp in length
* 50434 50533: gap of unknown length
* 50534 52880: contig of 2347 bp in length
* 52881 52980: gap of unknown length
* 52981 55194: contig of 2214 bp in length

* 55195 55294: gap of unknown length
* 55295 57482: contig of 2188 bp in length
* 57483 57582: gap of unknown length
* 57583 60781: contig of 3199 bp in length
* 60782 60881: gap of unknown length
* 60882 62599: contig of 1718 bp in length
* 62600 62699: gap of unknown length
* 62700 65203: contig of 2504 bp in length
* 65204 65303: gap of unknown length
* 65304 66914: contig of 1611 bp in length
* 66915 67014: gap of unknown length
* 67015 70839: contig of 3825 bp in length
* 70840 70939: gap of unknown length
* 70940 75139: contig of 4200 bp in length
* 75140 75239: gap of unknown length
* 75240 78296: contig of 3057 bp in length
* 78297 78396: gap of unknown length
* 78397 83138: contig of 4742 bp in length
* 83139 83238: gap of unknown length
* 83239 88204: contig of 4966 bp in length
* 88205 88304: gap of unknown length
* 88305 92238: contig of 3934 bp in length
* 92239 92338: gap of unknown length
* 92339 97339: contig of 5001 bp in length
* 97340 97439: gap of unknown length
* 97440 103534: contig of 6095 bp in length
* 103535 103634: gap of unknown length
* 103635 107080: contig of 3446 bp in length
* 107081 107180: gap of unknown length
* 107181 115201: contig of 8021 bp in length
* 115202 115301: gap of unknown length
* 115302 121237: contig of 5936 bp in length
* 121238 121337: gap of unknown length
* 121338 127910: contig of 6573 bp in length
* 127911 128010: gap of unknown length
* 128011 137964: contig of 9954 bp in length.
Location/Qualifiers
1. 137964
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-301E4"

BASE COUNT 31831 a 34027 c 35229 g 31979 t 4898 others
ORIGIN

Query Match 18.8% Score 166; DB 2; Length 137964;
Best Local Similarity 99.5% Pred. No. 1.3e-77;
Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAGCCTTGATCTCCAGAGGACCCCTGGGAGACAGGGCCCTGGCAAGCTGCAGCC 60
Db 74321 GACGCTTGATCTCCAGAGGACCCCTGGGAGACAGGGCCCTGGCAAGCTGCAGCC 74262
OY 61 GCTGGCAGTGGCTGGAATGAGGCTTTTAACTGGGAAGTGAAGAGGCTC 120
Db 74261 GCTGGCAGTGGCTGGAATGAGGCTTTTAACTGGGAAGTGAAGAGGCTC 74202
OY 121 CTGTCAGCTTGCTTAAGTCTTAGCACTTGCTGGCGTTGGCTTCACACACTGTGAGA 180
Db 74201 CTGTCAGCTTGCTTAAGTCTTAGCACTTGCTGGCGTTGGCTTCACACACTGTGAGA 74142
OY 181 CACCTTCGTGGTGGCTCCACGGCCTCACCTTCAGGT 217
Db 74141 CACCTTCGTGGTGGCTCCACGGCCTCACCTTCAGGT 74105

RESULT 4
AF259981 1741 bp mRNA linear ROD 09-MAY-2000
LOCUS AF259981
DEFINITION Rattus norvegicus CCN family protein COP-1 (Cop-1) mRNA, complete
cds.
ACCESSION AF259981
VERSION AF259981.1 GI:7739780
KEYWORDS

SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1741)
AUTHORS Zhang, R., Averboukh, L., Zhu, W., Zhang, H., Jo, H., Dempsey, P.J.,
Coffey, R.J., Pardee, A.B. and Liang, P.
TITLE Identification of rcop-1, a new member of the CCN protein family,
as a negative regulator for cell transformation
JOURNAL Mol. Cell. Biol. 18 (10), 6131-6141 (1998)
MEDLINE 98414629
PUBMED 9742130
REFERENCE 2 (bases 1 to 1741)
AUTHORS Liang, P.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer
Center, 649 MRB II, Nashville, TN 37232, USA
FEATURES
source
1. 1741
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
1. 1741
/gene="Cop-1"
262. 1014
/gene="Cop-1"
/note="secreted protein"
/codon_start=1
/product="CCN family protein COP-1"
/protein_id="AAF6901.1"
/db_xref="GI:7739781"
/translation="MRGSPILRLIATSFCLISMVCAQLCRTPCTCPWTPPQCPQGV
LVLDGCGCKVCARLRTESCEHLHYCERSQGLVQCQPGAPGCHGAVCLDEDGCEV
NGRRYLDGETEPKNCRLCRCDGFTCLPLCSEDTLPSMDCPRPKRIQVPGKCP
WVCDQVTPAIQSAAGHQLSALVTPASADAPWPNWSTAWGPCSTTCGLIATRVSN
QNRFCQLEIQRRLCLPRPCLAAARSHSSWNSAF"

BASE COUNT 386 a 491 c 480 g 384 t
ORIGIN
Query Match 13.3% Score 117; DB 10; Length 1741;
Best Local Similarity 99.1% Pred. No. 5.1e-51;
Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 665 GCTGCCAGCTGGGACTGCCACGCGCCCAAGAGATACAGGTGCCAGAAAGTGCTGCC 724
Db 678 GCTGCCAGCTGGGACTGCCACGCGCCCAAGAGATACAGGTGCCAGAAAGTGCTGCC 737
OY 725 CGAGTGGGTATGTACCAAGGAGTGAACACCGCGCATCCAGCGCTCCACGCGCAAGGACA 784
Db 738 CGAGTGGGTATGTACCAAGGAGTGAACACCGCGCATCCAGCGCTCCACGCGCAAGGACA 797
OY 785 CCACTTTCTGCCCTGTCTCACTCTGCTGCTGCTGATGCTCTCTTGTCCAAATTGGAGCAC 844
Db 798 CCACTTTCTGCCCTGTCTCACTCTGCTGCTGCTGATGCTCTCTTGTCCAAATTGGAGCAC 857
OY 845 AGCCTGGGGCCCTGCTCAACCAACCTGTGGGCTGGGCAT 883
Db 858 AGCCTGGGGCCCTGCTCAACCAACCTGTGGGCTGGGCAT 896

RESULT 5
AR210324 1734 bp DNA linear PAT 20-JUN-2002
LOCUS AR210324
DEFINITION Sequence 17 from patent US 6387657.
ACCESSION AR210324
VERSION AR210324.1 GI:21512525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Botstein, D.A., Cohen, R.L., Goddard, A.D., Gurney, A.L., Hillan, K.J.,
Lawrence, D.A., Levine, A.J., Pennica, D., Roy, M. Ann. and Wood, W.I.

TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 17 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..1734
/organism="unknown"
BASE COUNT 355 a 491 c 495 g 393 t
ORIGIN
Query Match 10.2%; Score 90; DB 6; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.4e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGCACGAGGCTGGGAGTCTCGACACCTGCATGTCTGCGACCCAGCCA 469
|||||
DB 418 AGTGTGTGCACGAGGCTGGGAGTCTCGACACCTGCATGTCTGCGACCCAGCCA 477

QY 470 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 499
|||||
DB 478 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 507

RESULT 6
AR210325/c 1734 bp DNA linear PAT 20-JUN-2002
LOCUS AR210325 Sequence 18 from patent US 6387657.
ACCESSION AR210325
VERSION AR210325.1 GI:21512526
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 18 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..1734
/organism="unknown"
BASE COUNT 393 a 495 c 491 g 355 t
ORIGIN
Query Match 10.2%; Score 90; DB 6; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.4e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGCACGAGGCTGGGAGTCTCGACACCTGCATGTCTGCGACCCAGCCA 469
|||||
DB 1317 AGTGTGTGCACGAGGCTGGGAGTCTCGACACCTGCATGTCTGCGACCCAGCCA 1258

QY 470 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 499
|||||
DB 1257 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 1228

RESULT 7
AF100778 1734 bp mRNA linear ROD 17-DEC-1998
LOCUS AF100778 Mus musculus connective tissue growth factor related protein wisp-2
DEFINITION (wisp2) mRNA, complete cds.
ACCESSION AF100778
VERSION AF100778.1 GI:4028578
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A.,
Lee,J., Brush,J., Taneyhill,L.A., Deuel,B., Lew,M., Watanabe,C.,
Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D.,
Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J.
WISP genes are members of the connective tissue growth factor
TITLE

family that are up-regulated in wnt-1-transformed cells and
aberrantly expressed in human colon tumors
Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
JOURNAL MEDLINE 99061933
PUBMED 9843955
REFERENCE 2 (bases 1 to 1734)
AUTHORS Pennica,D.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1998) Molecular Oncology, Genentech, Inc., 1 DNA
Way, South San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
source 1..1734
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="C57MG"
/cell_type="epithelial"
/tissue_type="mammary"
/note="transformed by wnt-1"
1..1734
/gene="Wisp2"
257..1012
/gene="Wisp2"
/codon_start=1
/product="connective tissue growth factor related protein
WISP-2"
/protein_id="AAC96320.1"
/db_xref="GI:4028579"
/translation="MRGNPLIHLAISFLCILSMVYSOLCPAPACAPMTPPQCPGPV
LYDGGCCGRCVRCARLGECDHLHVCDPGQGLVCPGAPSGRGAVCLFEEDGSCV
NGRRYLDETFKPNCRVLCRCDGFTCLPLCSEDPVRLPSWDCPRPRIQVGRCPB
WYCDQAVMQPAIQPSSAQGHQLSALVTPASADGPPPNWSTAWGPCSTTCGLGIATRV
NQNRFQLEIQRLCLSRPCLASRSHGWSNAF"
BASE COUNT 355 a 491 c 495 g 393 t
ORIGIN
Query Match 10.2%; Score 90; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.4e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGCACGAGGCTGGGGAGTCTCGACACCTGCATGTCTGCGACCCAGCCA 469
|||||
DB 418 AGTGTGTGCACGAGGCTGGGGAGTCTCGACACCTGCATGTCTGCGACCCAGCCA 477

QY 470 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 499
|||||
DB 478 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 507

RESULT 8
AL731698 61072 bp DNA linear ROD 24-MAY-2002
LOCUS AL731698 Mouse DNA sequence from clone RP23-161B3 on chromosome 2, complete
DEFINITION sequence.
ACCESSION AL731698
VERSION AL731698.10 GI:21214309
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 61072)
AUTHORS Wallis,J.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On May 25, 2002 this sequence version is compared from overlapping clones.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
COMMENT

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-161B3 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6.

FEATURES
source
1. .61072
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
/clone="RP23-161B3"
/clone_1lb="RPCI-23"
Location/Qualifiers

BASE COUNT 15405 a 15368 c 15033 g 15266 t
ORIGIN

Query Match 10.2%; Score 90; DB 10; Length 61072;
Best Local Similarity 100.0%; Pred. No. 7.1e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGACGAGCGCTGGGGAGTCTCGACACCTGCATGCTGCGACCCAGCCA 469
|||||

Db 10029 AGTGTGACGAGCGCTGGGGAGTCTCGACACCTGCATGCTGCGACCCAGCCA 10088
|||||

OY 470 GGGCCTGTTGTGACGCTGGGGCAGGCC 499
|||||

Db 10089 GGGCCTGTTGTGACGCTGGGGCAGGCC 10118
|||||

RESULT 9
AL669906 216757 bp DNA linear HTG 24-JUL-2002
LOCUS

DEFINITION Mus musculus chromosome 2 clone RP23-217C2, *** SEQUENCING IN
PROGRESS ***; 21 unordered pieces.

ACCESSION AL669906
VERSION AL669906.5 GI:21955520

KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.

SOURCE Mus musculus.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 216757)

AUTHORS Sims,S.

TITLE Direct Submission

JOURNAL

COMMENT

Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jul 25, 2002 this sequence version replaced gi:18181793.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bm217C2

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 211865 bases at least @40

Consensus quality: 213403 bases at least @30

Consensus quality: 214139 bases at least @20

Insert size: 214757; sum-of-contigs

Insert size: 234243; 1.8% error; agarose-ff

Quality coverage: 6.29x in Q20 bases; sum-of-contigs Quality
coverage: 5.90x in Q20 bases; agarose-ff

* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 4000: contig of 4000 bp in length
* 4001 4100: gap of 100 bp
* 4101 15267: contig of 11167 bp in length
* 15268 15367: gap of 100 bp
* 15368 34970: contig of 19603 bp in length
* 34971 35070: gap of 100 bp
* 35071 39671: contig of 4601 bp in length
* 39672 39771: gap of 100 bp
* 39772 46360: contig of 6589 bp in length
* 46361 46460: gap of 100 bp
* 46461 49809: contig of 3349 bp in length
* 49810 49909: gap of 100 bp
* 49910 54509: contig of 4600 bp in length
* 54510 54609: gap of 100 bp
* 54610 65989: contig of 11380 bp in length
* 65990 66089: gap of 100 bp
* 66090 84635: contig of 18546 bp in length
* 84636 84735: gap of 100 bp
* 84736 87399: contig of 2664 bp in length
* 87400 87499: gap of 100 bp
* 87500 98601: contig of 11102 bp in length
* 98602 98701: gap of 100 bp
* 98702 105522: contig of 6821 bp in length
* 105523 105622: gap of 100 bp
* 105623 119773: contig of 14151 bp in length
* 119774 119873: gap of 100 bp
* 119874 134552: contig of 14679 bp in length
* 134553 134652: gap of 100 bp
* 134653 141202: contig of 6550 bp in length
* 141203 141302: gap of 100 bp
* 141303 145808: contig of 4506 bp in length
* 145809 145908: gap of 100 bp
* 145909 151572: contig of 5664 bp in length
* 151573 151672: gap of 100 bp
* 151673 169686: contig of 18014 bp in length
* 169687 169786: gap of 100 bp
* 169787 200095: contig of 30309 bp in length
* 200096 200195: gap of 100 bp
* 200196 213877: contig of 13682 bp in length
* 213878 213977: gap of 100 bp
* 213978 216757: contig of 2780 bp in length.

FEATURES
source
1. .216757
Location/Qualifiers

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="2"

/clone="RP23-217C2"

/clone_1lb="RPCI-23"

1. .4000

/note="assembly_fragment:03429"

clone_end:SP6

vector_side:left

4101. .15267

/note="assembly_fragment:00814"

fragment_chain:1

15368. .34970

/note="assembly_fragment:00812"

fragment_chain:1

35071. .39671

/note="assembly_fragment:03544"

fragment_chain:1

39772. .46360

misc_feature /note="assembly_fragment:01438
fragment_chain:1"
46461. .49809
/note="assembly_fragment:03410
fragment_chain:2"
49910. .54509
/note="assembly_fragment:00811
fragment_chain:2"
54610. .65989
/note="assembly_fragment:02217
fragment_chain:2"
66090. .84635
/note="assembly_fragment:03529
fragment_chain:2"
84736. .87399
/note="assembly_fragment:01019
fragment_chain:3"
87500. .98601
/note="assembly_fragment:01170
fragment_chain:3"
98702. .105522
/note="assembly_fragment:02829
fragment_chain:3"
105623. .119773
/note="assembly_fragment:01476
fragment_chain:4"
119874. .134552
/note="assembly_fragment:00505
fragment_chain:4"
134653. .141202
/note="assembly_fragment:01951
fragment_chain:4"
141303. .145808
/note="assembly_fragment:02637
fragment_chain:5"
145909. .151572
/note="assembly_fragment:02352
fragment_chain:5"
151673. .169686
/note="assembly_fragment:02207
fragment_chain:5"
169787. .200095
/note="assembly_fragment:02849
fragment_chain:6"
200196. .213877
/note="assembly_fragment:01052
fragment_chain:6"
213978. .216757
/note="assembly_fragment:01318
clone_end:T7
vector_side:right"
BASE COUNT 56425 a 51573 c 51904 g 54852 t 2003 others
ORIGIN
Query Match 10.2%; Score 90; DB 2; Length 216757;
Best Local Similarity 100.0%; Pred. No. 5.6e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 410 AGTGTGTGACGAGGCTGGGGAGTCTGCGACACCTGCATGTCTGCGACCCAGCCA 469
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Db 166450 AGTGTGTGACGAGGCTGGGGAGTCTGCGACACCTGCATGTCTGCGACCCAGCCA 166509
QY 470 GGGCCTGTTGTGACGCTGGGGCAGGCC 499
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Db 166510 GGGCCTGTTGTGACGCTGGGGCAGGCC 166539

RESULT 10
AF126063 1739 bp mRNA linear ROD 12-OCT-1999
LOCUS AF126063
DEFINITION Mus musculus connective tissue growth factor-like protein precursor
(Ctgf1) mRNA, complete cds.
ACCESSION AF126063

VERSION AF126063.1 GI:4337059
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1739)
AUTHORS Kumar,S., Hand,A.T., Connor,J.R., Dodds,R.A., Ryan,P.J.,
Trill,J.J., Fisher,S.M., Nuttall,M.E., Lipschutz,D.B., Zou,C.,
Hwang,S.M., Volta,B.J., James,I.E., Rleman,D.J., Gowen,M. and
Lee,J.C.
TITLE Identification and cloning of a connective tissue growth
factor-like cDNA from human osteoblasts encoding a novel regulator
of osteoblast functions
JOURNAL J. Biol. Chem. 274 (24), 17123-17131 (1999)
MEDLINE 99287915
PUBMED 10358067
REFERENCE 2 (bases 1 to 1739)
AUTHORS Kumar,S. and Zou,C.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1999) Bone & Cartilage Biology, UW 2109,
Smithkline Beecham, 709 Swedeland Rd., King of Prussia, PA 19406,
USA

FEATURES
source Location/Qualifiers
1. .1739
/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="lung"
1. .1739
/gene="Ctgf1"
242. .997
/gene="Ctgf1"
/note="similar to the Mus musculus WISP-2 protein encoded
by the sequence presented in GenBank Accession Number
AF100778; putative growth factor; CTGF-L; contains IGF
binding (IGFBP), Von Willebrand Factor type C (VWC) repeat
and thrombospondin type I (TSP1) domains; member of the
CCN (CTGF/Cyrl/Nov) family; lacks the fourth
carboxy-terminal (CT) domain present in other members of
the CCN family"
/codon_start=1
/product="connective tissue growth factor-like protein
precursor"
/protein_id="AAD18058.1"
/db_xref="GI:4337060"
/translation="MRGNPLIHLLAISFLCILSMVYSQICPAPCACPWTPPOCPGVP
LVLDGCGCCRCVRCARLGESEDLHVCDPQSGLVCQPGAGSGRGAVCLFEEDGSCV
NGRRYLDETFEFPNCRVLCRCDDGFTCLPICESEDVRLPSWDPCPRRIQVGRCP
WVCQAVMQPAIQPSSAQGHQLSALVTPASADGPPCWNWSTAWGPCSTTCGLGIATRV
NNRFCOLEIQRLCLSRPCLASRSHGWSNSAF"

BASE COUNT 375 a 480 c 489 g 395 t
ORIGIN
Query Match 9.1%; Score 80; DB 10; Length 1739;
Best Local Similarity 100.0%; Pred. No. 3.2e-31;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 420 CGGAGCTGGGGAGTCTGCGACACCTGCATGTCTGCGACCCAGGGCGTGT 479
|||||
Db 413 CGGAGCTGGGGAGTCTGCGACACCTGCATGTCTGCGACCCAGGGCGTGT 472
QY 480 TGTCAAGCCTGGGGCAGGCC 499
|||||
Db 473 TGTCAAGCCTGGGGCAGGCC 492

RESULT 11
AR210337 738 bp DNA linear PAT 20-JUN-2002
LOCUS AR210337
DEFINITION Sequence 38 from patent US 6387657.
ACCESSION AR210337
VERSION AR210337.1 GI:21512542
KEYWORDS

SOURCE unknown.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 738)
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M. Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 38 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..738
BASE COUNT 104 a 272 c 238 g 124 t
ORIGIN

Query Match 3.6%; Score 32; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGGATGGCTGTGGCTGCTG 406
Db 115 GTACCCCTGGTGGCTGGATGGCTGTGGCTGCTG 146

RESULT 12
LOCUS AR210338 841 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 39 from patent US 6387657.
ACCESSION AR210338
VERSION AR210338.1 GI:21512543
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 841)
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M. Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 39 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..841
BASE COUNT 124 a 297 c 280 g 140 t
ORIGIN

Query Match 3.6%; Score 32; DB 6; Length 841;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 685
Db 417 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 448

RESULT 13
LOCUS AX076919 1266 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 31 from Patent WO0105836.
ACCESSION AX076919
VERSION AX076919.1 GI:13121575
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and
Wood,W.I.
TITLE Polypeptidic compositions and methods for the treatment of tumors
JOURNAL Patent: WO 0105836-A 31 25-JAN-2001;
FEATURES Location/Qualifiers
source 1..1266
/organism="Homo sapiens"

BASE COUNT 216 a 418 c 390 g 242 t
ORIGIN /db_xref="taxon:9606"

Query Match 3.6%; Score 32; DB 6; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGGATGGCTGTGGCTGCTG 406
Db 136 GTACCCCTGGTGGATGGCTGTGGCTGCTG 167

RESULT 14
LOCUS AX464186 1266 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 319 from Patent WO0140466.
ACCESSION AX464186
VERSION AX464186.1 GI:21899109
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 319 07-JUN-2001;
FEATURES Location/Qualifiers
source 1..1266
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 216 a 418 c 390 g 242 t
ORIGIN

Query Match 3.6%; Score 32; DB 6; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGGTGGATGGCTGTGGCTGCTG 406
Db 136 GTACCCCTGGTGGATGGCTGTGGCTGCTG 167

RESULT 15
LOCUS AF083500 1283 bp mRNA linear PRI 04-NOV-1998
DEFINITION Homo sapiens connective tissue growth factor-like protein
precursor, mRNA, complete cds.
ACCESSION AF083500
VERSION AF083500.1 GI:3462835
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Kumar,S., Hand,A.T., Connor,J.C., Dodds,R.A., Ryan,P.J.,
Trill,J.G., Fisher,S.M., Slemmon,J.R., Lipshutz,D.B.,
Bartholomew,V., James,I.E., Rleman,D.J., Gowen,M. and Lee,J.C.
TITLE Identification and cloning of CTGF-L from human osteoblasts, a
novel cysteine rich protein containing an IGF binding domain
JOURNAL Bone 23 (5), S240 (1998)
REFERENCE 2 (bases 1 to 1283)
AUTHORS Kumar,S.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1998) Bone & Cartilage Biology, UW 2109,
SmithKline Beecham, 709 Swedeland Road, King of Prussia, PA 19406,

FEATURES USA

source

1. .1283 location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="20"

/map="20q12-q13"

/cell_type="primary osteoblast"

9. .761

/note="CTGF-L; encodes IGF binding (IGFB), Von Willebrand factor type C (VWC) and thrombospondin type I (TSP1) domains; member of the CCN (CTGF/cyrl/nov) family; lacks the fourth carboxy-terminal domain present in other members of the CCN family"

/codon_start=1

/product="connective tissue growth factor-like protein precursor"

/protein_id="AAC70350.1"

/db_xref="GI:3462836"

/translation="MRGTPKTHLLAFSLCLLSKVRNQLCPTPCTCPWPPPRCDLGVPLVLDGCGCCRVCAARRLGEPCDQLHVCDAQGLVCPGAGPGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRRCEDGGFTCVPLCSSEVRLPSWDCPHPRRVEVLGKCCPEWCGGGGLGTQPLPAQGPQFSGLVSSLPGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLTQRLCLSRPCPPSRGRSPQNSAF"

BASE COUNT 235 a 418 c 389 g 241 t

ORIGIN

Query Match 3.6%; Score 32; DB 9; Length 1283;

Best Local Similarity .100.0%; Pred. No. 1.6e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 GTACCCCTGCTGCTGGATGGCTGCTGCTG 406

|||||

Db 135 GTACCCCTGCTGCTGGATGGCTGCTGCTG 166

Search completed: July 28, 2003, 21:14:41

Job time : 2455.86 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:31:11 ; Search time 231.91 Seconds
(without alignments)
8574.520 Million cell updates/sec

Title: US-10-010-408-1_COPY_1_883
Perfect score: 883
Sequence: 1 GACGCTTCGATCTCCAGAG.....ACCACCTGTGGCTGGGCAT 883

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 segs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseg/genesegn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	883	100.0	1708	20	AAZ07516 Rat HICP polypepti
2	635	71.9	753	20	AAZ07517 Rat HICP polypepti
3	566	64.1	681	20	AAZ07521 Rat HICP mature po
4	210	23.8	210	20	AAZ07519 Rat HICP IGFBP dom
5	177	20.0	177	20	AAZ07518 Rat HICP VWC domai
6	90	10.2	753	20	AAZ07518 Rat HICP VWC domai
7	90	10.2	753	20	AAZ07518 Rat HICP VWC domai
8	59	6.7	1734	20	AAZ07520 Mouse WISP-2 prote
9	32	3.6	199	22	ABA72245 Rat HICP TSPI doma
					Human foetal liver

10	32	3.6	199	22	ABA38112	Probe #16578 for g
11	32	3.6	199	22	AAK20667	Human brain expres
12	32	3.6	199	22	AAK46811	Human bone marrow
13	32	3.6	199	22	AAI25749	Probe #15682 for g
14	32	3.6	199	22	AAI52650	Probe #21336 used
15	32	3.6	199	24	ABS21124	Human genome-deriv
16	32	3.6	586	22	ABA59703	Human foetal liver
17	32	3.6	586	22	ABA28232	Probe #6698 for ge
18	32	3.6	586	22	AAK07972	Human bone expres
19	32	3.6	586	22	AAK33842	Human bone marrow
20	32	3.6	586	22	AAI16552	Probe #6485 for ge
21	32	3.6	586	22	AAI39568	Probe #8254 used t
22	32	3.6	586	24	ABS08689	Human genome-deriv
23	32	3.6	738	20	AAZ07501	Human WISP-2 prote
24	32	3.6	750	20	AAZ07501	Human WISP-2 prote
25	32	3.6	841	20	AAZ07502	Human WISP-2 prote
26	32	3.6	1257	20	AAZ07502	EGF-like homologue
27	32	3.6	1266	21	AAA30048	Human PRO261 nucle
28	32	3.6	1266	22	AAZ21403	Human CDNA sequenc
29	32	3.6	1266	22	AAZ07506	PRO261 coding sequ
30	32	3.6	1266	22	AAZ07506	Human angiotensin
31	32	3.6	1267	21	AAZ07506	Human PRO261 CDNA
32	32	3.6	1285	19	AAZ07506	Human connective t
33	32	3.6	1293	20	AAZ07506	Human WISP-2 prote
34	32	3.6	1309	22	AAH28214	Connective tissue
35	32	3.6	1337	22	AAH46952	Human secreted pro
36	32	3.6	1352	22	AAH46936	Human secreted pro
37	32	3.6	1522	20	AAH16595	Human growth facto
38	32	3.6	2136	22	AAK94706	Human full-length
39	32	3.6	13255	22	AAK76842	Human immune/haema
40	27	3.1	51	20	AAZ07535	Human WISP-2 prote
41	27	3.1	51	21	AAZ07569	Human PRO261 hybr
42	27	3.1	51	21	AAZ07569	Human PRO261 hybr
43	27	3.1	51	22	AAZ07569	Probe for PRO261 n
44	27	3.1	51	22	AAZ07569	PRO261 probe #1.
45	23	2.6	634	22	AAK91750	Human PRO261 hybr
						Human CDNA 5'-end

ALIGNMENTS

RESULT 1	
AAZ07516	
ID	AAZ07516 standard; CDNA: 1708 BP.
XX	
AC	AAZ07516;
XX	
DT	26-NOV-1999 (first entry)
XX	
DE	Rat HICP polypeptide encoding CDNA.
XX	
KW	Heparin-induced CCN-like protein; HICP: cell-associated activity; ss;
KW	cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
XX	
OS	Rattus sp.
XX	
PN	W09947556-A2.
XX	
PD	23-SEP-1999.
XX	
PF	18-MAR-1999; 99WO-US05999.
XX	
PR	19-MAR-1998; 98US-0044273.
XX	
PA	(TUFT) TUFTS COLLEGE.
XX	
PI	Castellot JJ;
XX	
DR	WPI, 1999-562060/47.
DR	P-PSDB; AAY27434.
XX	
PT	Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
PT	used in methods to identify modulators or in diagnostic applications

Db 181 GGGAGTCTCTGCACACCACTGCATGTCTGCCAGCCCAAGCCAGGGCCTGGTTGTACAGCCT 240
QY 489 GGGGACGGCCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGATGACGGTAGCTGT 548
Db 241 GGGGACGGCCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGATGACGGTAGCTGT 300
QY 549 GAGGTGAATGGCCGAGGTACCTGGATGAGAGACCTTTAAACCAATTGCAGGGTCTG 608
Db 301 GAGGTGAATGGCCGAGGTACCTGGATGAGAGACCTTTAAACCAATTGCAGGGTCTG 360
QY 609 TGGCGCTGTGATGACGGGTGGCTTACCTGCCCTGCGCTGTGCAGTGAAGATGTGCGGCTG 668
Db 361 TGCCGCTGTGATGACGGGTGGCTTACCTGCCCTGCGCTGTGCAGTGAAGATGTGCGGCTG 420
QY 669 CCCAGCTGGAGCTGCCACGCGCCCAAGAGAATACAGGTGCCAAGAAAGTCTGCCCGAG 728
Db 421 CCCAGCTGGAGCTGCCACGCGCCCAAGAGAATACAGGTGCCAAGAAAGTCTGCCCGAG 480
QY 729 TGGGTATGTGACCAAGGAGTGCACACCGCGATCCAGCGCTCCAGCGCAAGACACCAA 788
Db 481 TGGGTATGTGACCAAGGAGTGCACACCGCGATCCAGCGCTCCAGCGCAAGACACCAA 540
QY 789 CTTTCTGCGCTTGTCACTCCTGCTGCTGTGATGCTCTTGTCCAAATTGAGACACAGCC 848
Db 541 CTTTCTGCGCTTGTCACTCCTGCTGCTGTGATGCTCTTGTCCAAATTGAGACACAGCC 600
QY 849 TGGGGCCCTGCTCAACCACTGTGGGCTGGGCAT 883
Db 601 TGGGGCCCTGCTCAACCACTGTGGGCTGGGCAT 635

RESULT 3
AAZ07521
ID AAZ07521 standard; cDNA; 681 BP.

AC AAZ07521;
DT 26-NOV-1999 (first entry)

DE Rat HICP mature polypeptide coding sequence.

KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;
KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.

OS Rattus sp.

PN MO9947556-A2.

PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-US05999.

PR 19-MAR-1998; 98US-0044273.

PA (TUFT) TUFTS COLLEGE.

PI Castellot JJ;

DR WPI; 1999-562060/47.

DR P-PSDB; AAY27440.

PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
used in methods to identify modulators or in diagnostic applications
PS Disclosure; Fig 2; 108pp; English.

CC The invention provides a rat heparin-induced CCN-like protein (HICP)
CC protein. Agents that stimulate or inhibit HICP protein activity or
CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
CC can be used to modulate cell-associated activity. HICP modulators can be
CC used to treat disorders characterized by aberrant HICP protein activity
CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
CC specific for HICP can be used to detect HICP activity in a biological

CC sample. HICP can be used to treat disorders, such as a cardiovascular or
CC fibrotic disorder, characterized by aberrant cell proliferation. The
CC present sequence represents the coding sequence of rat HICP mature
CC polypeptide.

SO Sequence 681 BP; 121 A; 211 C; 215 G; 134 T; 0 other;

Query Match 64.1%; Score 566; DB 20; Length 681;
Best Local Similarity 100.0%; Pred. No. 1.1e-259;
Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 CAGCTGTGCCGGACACCCCTGTACTGTCTTGACACACCAACCCAGTGCACAGGGGTA 377
Db 1 CAGCTGTGCCGGACACCCCTGTACTGTCTTGACACACCAACCCAGTGCACAGGGGTA 60
QY 378 CCCCTGTGCTGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGAGGCTGGGAGTCC 437
Db 61 CCCCTGTGCTGATGGCTGTGGCTGCTGTAAAGTGTGTGCACGAGGCTGGGAGTCC 120
QY 438 TGGACACCACTGCATGTCTGCGACCCCAAGCCAGGGCCTGTTGTACAGCCTGGGCAAGC 497
Db 121 TGGACACCACTGCATGTCTGCGACCCCAAGCCAGGGCCTGTTGTACAGCCTGGGCAAGC 180
QY 498 CTTGGCGGCATGGGGCTGTGTCTTGTGATGAGGATGACGGTAGCTGTGAGTGAAT 557
Db 181 CTTGGCGGCATGGGGCTGTGTCTTGTGATGAGGATGACGGTAGCTGTGAGTGAAT 240
QY 558 GGCCGAGGTACCTGGATGAGAGACCTTTAAACCAATTGCAGGCTCTGTGCCGCTGT 617
Db 241 GGCCGAGGTACCTGGATGAGAGACCTTTAAACCAATTGCAGGCTCTGTGCCGCTGT 300
QY 618 GATGACGGTGTCTTACCTGCTGCCCTGTGCAAGTGAAGATGCGGCTGCCAGCTGG 677
Db 301 GATGACGGTGTCTTACCTGCTGCCCTGTGCAAGTGAAGATGCGGCTGCCAGCTGG 360
QY 678 GACTGCCACGCGCCCAAGAGAATACAGTGCAGGAAGTGTGCCCGGAGTGGTATGT 737
Db 361 GACTGCCACGCGCGCCCAAGAGAATACAGTGCAGGAAGTGTGCCCGGAGTGGTATGT 420
QY 738 GACCAGGAGTGCACACCGGCGATCCAGCGCTCCAGCGCAAGGACACCACTTCTGCC 797
Db 421 GACCAGGAGTGCACACCGGCGATCCAGCGCTCCAGCGCAAGGACACCACTTCTGCC 480
QY 798 CTTGTCACTCTGCCCTGTGCTGATGCTCTTGTCCAAATTGAGACACAGCCTGGGGCCCC 857
Db 481 CTTGTCACTCTGCCCTGTGCTGATGCTCTTGTCCAAATTGAGACACAGCCTGGGGCCCC 540
QY 858 TGCTCAACCACTGTGGGCTGGGCAT 883
Db 541 TGCTCAACCACTGTGGGCTGGGCAT 566

RESULT 4
AAZ07519
ID AAZ07519 standard; cDNA; 210 BP.

AC AAZ07519;

DT 26-NOV-1999 (first entry)

DE Rat HICP IGFBP domain encoding cDNA.

KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;
KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;

KW insulin-like growth factor binding protein; IGFBP.

OS Rattus sp.

PN WO9947556-A2.

PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-US05999.

XX 19-MAR-1998; 98US-0044273.
 XX (TUFT) TUFTS COLLEGE.
 XX Castellot JJ;
 XX WPI: 1999-562060/47.
 DR P-PSDB; AAY27438.
 XX Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
 PT used in methods to identify modulators or in diagnostic applications
 XX
 PS Disclosure; Page 104; 108bp; English.
 XX The invention provides a rat heparin-induced CCN-like protein (HICP)
 CC protein. Agents that stimulate or inhibit HICP protein activity or
 CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
 CC can be used to modulate cell-associated activity. HICP modulators can be
 CC used to treat disorders characterized by aberrant HICP protein activity
 CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
 CC specific for HICP can be used to detect HICP activity in a biological
 CC sample. HICP can be used to treat disorders, such as a cardiovascular or
 CC fibrotic disorder, characterized by aberrant cell proliferation. The
 CC present sequence represents a nucleotide sequence encoding the insulin-
 CC like growth factor binding protein (IGFBP) domain of HICP polypeptide.
 XX
 SQ Sequence 210 BP; 27 A; 65 C; 74 G; 44 T; 0 other;

Query Match 23.8%; Score 210; DB 20; Length 210;
 Best Local Similarity 100.0%; Pred. No. 5.2e-90;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 318 CAGCTGTGCCGACACCCCTGTACCTGTCTGACACACACACCCAGTGCACACAGGGGTA 377
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CAGCTGTGCCGACACCCCTGTACCTGTCTGACACACACACCCAGTGCACACAGGGGTA 60
 OY 378 CCCCTGTGTGATGCTGTGCTGTGCTGTGTAAGTGTGACAGGAGGCTGGGGAGTCC 437
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CCCCTGTGTGATGCTGTGCTGTGCTGTGTAAGTGTGACAGGAGGCTGGGGAGTCC 120
 OY 438 TGGACACACCTGATGTGTGCGACCCAGCCAGGCGCTGTTGTGACGCTGGGGCAGGC 497
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 TGGACACACCTGATGTGTGCGACCCAGCCAGGCGCTGTTGTGACGCTGGGGCAGGC 180
 OY 498 CCTGGCGGCATGGGCTGTGTCTCTTG 527
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CCTGGCGGCATGGGCTGTGTCTCTTG 210

RESULT 5
 AAZ07518
 ID AAZ07518 standard; cDNA; 177 BP.
 XX
 AC AAZ07518;
 XX
 DT 26-NOV-1999 (first entry)
 XX
 DE Rat HICP VWC domain encoding cDNA.
 XX
 KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;
 KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;
 KW Von Willebrand C domain; VWC.
 XX
 OS Rattus sp.
 XX
 PN WO9947556-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-US05999.
 XX
 PR 19-MAR-1998; 98US-0044273.

XX (TUFT) TUFTS COLLEGE.
 XX Castellot JJ;
 XX WPI: 1999-562060/47.
 DR P-PSDB; AAY27436.
 XX Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
 PT used in methods to identify modulators or in diagnostic applications
 XX
 PS Disclosure; Page 103; 108bp; English.
 XX The invention provides a rat heparin-induced CCN-like protein (HICP)
 CC protein. Agents that stimulate or inhibit HICP protein activity or
 CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
 CC can be used to modulate cell-associated activity. HICP modulators can be
 CC used to treat disorders characterized by aberrant HICP protein activity
 CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
 CC specific for HICP can be used to detect HICP activity in a biological
 CC sample. HICP can be used to treat disorders, such as a cardiovascular or
 CC fibrotic disorder, characterized by aberrant cell proliferation. The
 CC present sequence represents a cDNA encoding the Von Willebrand C (VWC)
 CC a domain of the HICP polypeptide.
 XX
 SQ Sequence 177 BP; 35 A; 47 C; 60 G; 35 T; 0 other;

Query Match 20.0%; Score 177; DB 20; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.8e-74;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 TGTGAGTGAATGCGCCGACGAGTACCTGATGAGAGACCTTAAACCAATTGCAGGTC 605
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 TGTGAGTGAATGCGCCGACGAGTACCTGATGAGAGACCTTAAACCAATTGCAGGTC 60
 OY 606 CTGTGCCCTGTGATGACGGTGTGCTTACCTGCTGCGCTGTGACGTGAGATGTGCGG 665
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CTGTGCCCTGTGATGACGGTGTGCTTACCTGCTGCGCTGTGACGTGAGATGTGCGG 120
 OY 666 CTGCCACGCTGGGACTGCCACGCCCCCAAGAGAATACAGGTGCCAGAAAGTGCTGC 722
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CTGCCACGCTGGGACTGCCACGCCCCCAAGAGAATACAGGTGCCAGAAAGTGCTGC 177

RESULT 6
 AAX76489/c
 ID AAX76489 standard; DNA; 753 BP.
 XX
 AC AAX76489;
 XX
 DT 06-AUG-1999 (first entry)
 XX
 DE Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18.
 XX
 KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
 KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
 KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;
 KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
 KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
 KW connective tissue disorder; catabolic state; inflammation;
 KW testicular-related disorder; angiogenesis; immunological disorder; ss.
 XX
 OS Mus sp.
 XX
 PN WO9921998-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 29-OCT-1998; 98WO-US22991.
 XX
 PR 14-APR-1998; 98US-0081695.
 PR 29-OCT-1997; 97US-0063704.
 PR 03-FEB-1998; 98US-0073612.

```
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX
DR WPI; 1999-337420/28.
XX
PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
XX
PS Disclosure; Page 179-180; 284pp; English.
XX
CC The present invention describes Wnt-1 induced secreted polypeptides,
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
CC and WISP-3 have homology to connective tissue growth factor (CTGF).
CC Products from the present invention can be used to treat WISP-related
CC disorders such as breast, ovarian, and colon cancer or melanoma. The
CC products can be used to treat arteriosclerosis. The products can also be
CC used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and
CC blastocoelel disorders, haematopoesis-related disorders, tissue-growth
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
CC cells.
XX
SQ Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;

Query Match
Best Local Similarity 10.2%; Score 90; DB 20; Length 753;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGCACGAGGCTGGGGAGTCTTCGACACCTGCATGTCTGCGACCCAGCCA 469
Db 592 AGTGTGTGCACGAGGCTGGGGAGTCTTCGACACCTGCATGTCTGCGACCCAGCCA 533
QY 470 GGGCCTGCTTGTCTCAGCCTGGGGCAGGCC 499
Db 532 GGGCCTGCTTGTCTCAGCCTGGGGCAGGCC 503

RESULT 7
AAZ076488
ID AAX76488 standard; DNA; 1734 BP.
XX
AC AAX76488;
XX
DT 06-AUG-1999 (first entry)
XX
DE Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17.
XX
KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
KW leukaemia; lymphoid malignancy; haematopoesis-related disorder;
KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
KW connective tissue disorder; catabolic state; inflammation;
KW testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
OS Mus sp.
XX
PN W09921998-A1.
XX
PD 06-MAY-1999.
XX
PF 29-OCT-1998; 98WO-US22991.
```

```
XX
PR 14-APR-1998; 98US-0081695.
PR 29-OCT-1997; 97US-0063704.
PR 03-FEB-1998; 98US-0073612.
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX
DR WPI; 1999-337420/28.
XX
DR P-PSDB; AAY17651.
XX
PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
XX
PS Example 2; Page 178-179; 284pp; English.
XX
CC The present invention describes Wnt-1 induced secreted polypeptides,
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
CC and WISP-3 have homology to connective tissue growth factor (CTGF).
CC Products from the present invention can be used to treat WISP-related
CC disorders such as breast, ovarian, and colon cancer or melanoma. The
CC products can be used to treat arteriosclerosis. The products can also be
CC used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and
CC blastocoelel disorders, haematopoesis-related disorders, tissue-growth
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
CC cells.
XX
SQ Sequence 1734 BP; 355 A; 491 C; 495 G; 393 T; 0 other;

Query Match
Best Local Similarity 10.2%; Score 90; DB 20; Length 1734;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGTGCACGAGGCTGGGGAGTCTTCGACACCTGCATGTCTGCGACCCAGCCA 469
Db 418 AGTGTGTGCACGAGGCTGGGGAGTCTTCGACACCTGCATGTCTGCGACCCAGCCA 477
QY 470 GGGCCTGCTTGTCTCAGCCTGGGGCAGGCC 499
Db 478 GGGCCTGCTTGTCTCAGCCTGGGGCAGGCC 507

RESULT 8
AAZ07520
ID AAZ07520 standard; cDNA; 174 BP.
XX
AC AAZ07520;
XX
DT 26-NOV-1999 (first entry)
XX
DE Rat HICP TSPI domain encoding cDNA.
XX
KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;
KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;
KW thrombospondin 1 domain; TSPI.
XX
OS Rattus sp.
XX
PN W09947556-A2.
XX
PD 23-SEP-1999.
XX
```


PF 18-MAR-1999; 99WO-US05999.
XX
PR 19-MAR-1998; 98US-0044273.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Castellot JJ;
XX
DR WPI; 1999-562060/47.
DR P-PSDB; AAY27439.
XX
PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
PT used in methods to identify modulators or in diagnostic applications -
XX
PS Disclosure; Page 105; 108pp; English.
XX
CC The invention provides a rat heparin-induced CCN-like protein (HICP)
CC protein. Agents that stimulate or inhibit HICP protein activity or
CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
CC can be used to modulate cell-associated activity. HICP modulators can be
CC used to treat disorders characterized by aberrant HICP protein activity
CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
CC specific for HICP can be used to detect HICP activity in a biological
CC sample. HICP can be used to treat disorders, such as a cardiovascular or
CC fibrotic disorder, characterized by aberrant cell proliferation. The
CC present sequence represents a nucleotide sequence encoding the
CC thrombospondin 1 (TSP1) domain of the HICP polypeptide.
XX
SQ Sequence 174 BP; 36 A; 62 C; 45 G; 31 T; 0 other;

Query Match 6.7%; Score 59; DB 20; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.8e-18;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 825 CCTGTCCAAATGGAGCACAGCCTGGGCCCCCTGCTCAACCACTGTGGCTGGGCAT 883
DB 1 CCTGTCCAAATGGAGCACAGCCTGGGCCCCCTGCTCAACCACTGTGGCTGGGCAT 59

RESULT 9
ABA72245
ID ABA72245 standard; DNA; 199 BP.
XX
AC ABA72245;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #20550.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO20015727-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS Claim 4; SEQ ID NO 20550; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match 3.6%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 654 GAGGATGTGGGCTGCCAGCTGGGACTGCC 685
DB 129 GAGGATGTGGGCTGCCAGCTGGGACTGCC 160

RESULT 10
ABA38112
ID ABA38112 standard; DNA; 199 BP.
XX
AC ABA38112;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #16578 for gene expression analysis in human heart cell sample.
XX
DE Human; gene expression; heart; microarray; vascular system; probe;
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO20015727-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 4; SEQ ID NO 16578; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SO Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match 3.6%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 654 GAGGATGCGGCTGCCAGCTGGACTGCC 685

Db 129 GAGGATGCGGCTGCCAGCTGGACTGCC 160

RESULT 11

AAK20667

ID AAK20667 standard; DNA; 199 BP.

AC AAK20667;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 20658.

KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer; ss.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human

PT brains -

PS Example 4; SEQ ID NO: 20658; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention.
XX
XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

OY 654 GAGGATGCGGCTGCCAGCTGGACTGCC 685
|||||
Db 129 GAGGATGCGGCTGCCAGCTGGACTGCC 160

RESULT 12

AAK46811

ID AAK46811 standard; DNA; 199 BP.

AC AAK46811;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 21368.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

PS Example 4; SEQ ID NO: 21368; 658pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is one of

CC the probes of the invention.
XX
XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

OY 654 GAGGATGCGGCTGCCAGCTGGACTGCC 685
|||||
Db 129 GAGGATGCGGCTGCCAGCTGGACTGCC 160

RESULT 13

AAI25749

ID AAI25749 standard; DNA; 199 BP.

AC AAI25749;

DT 12-OCT-2001 (first entry)

DE Probe #15682 for gene expression analysis in human cervical cell sample.

XX
XX

KW Probe: human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID NO 15682; 487bp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SEN). The present sequence is one such probe. The SENs are derived
CC from human HeLa cells. The SENs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
XX
Query Match 3.6%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 654 GAGGATGTGGCGCTGCCAGCTGGAGCTGCC 685
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 129 GAGGATGTGGCGCTGCCAGCTGGAGCTGCC 160
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
RESULT 14
AAI52650
ID AAI52650 standard; DNA; 199 BP.
XX
AC AAI52650;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #21336 used to measure gene expression in human placenta sample.
XX
KW Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PA

PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID NO 21336; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SEN).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
XX
Query Match 3.6%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 654 GAGGATGTGGCGCTGCCAGCTGGAGCTGCC 685
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 129 GAGGATGTGGCGCTGCCAGCTGGAGCTGCC 160
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
RESULT 15
ABS21124
ID ABS21124 standard; DNA; 199 BP.
XX
AC ABS21124;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 21115.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tubercous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.

PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -

PS Claim 4; SEQ ID NO 21115; 634pp; English.

CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Kargener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a single exon
 CC probe open reading frame of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match 3.6%; Score 32; DB 24; Length 199;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGGATGTGGGCTGCCAGCTGGGACTGCC 685
 ||||||||||||||||||||||||||||||||
 Db 129 GAGGATGTGGGCTGCCAGCTGGGACTGCC 160

Search completed: July 28, 2003, 15:54:56
 Job time : 232.91 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:50:06 ; Search time 48.2525 Seconds
(without alignments)
5612.050 Million cell updates/sec

Title: US-10-010-408-1_COPY_1_883
Perfect score: 883
Sequence: 1 GACGCTTCTGATCTCCAGAG.....ACCACCTGTGGCTGGGCAT 883

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA:*
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3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	90	10.2	1734	4	US-09-182-145-17 Sequence 17, Appl
2	90	10.2	1734	4	US-09-182-145-18 Sequence 18, Appl
3	32	3.6	738	4	US-09-182-145-38 Sequence 38, Appl
4	32	3.6	841	4	US-09-182-145-39 Sequence 39, Appl
5	32	3.6	1293	4	US-09-182-145-13 Sequence 13, Appl
6	32	3.6	1293	4	US-09-182-145-14 Sequence 14, Appl
7	27	3.1	51	4	US-09-182-145-117 Sequence 117, App
8	19	2.2	616	4	US-09-385-982-220 Sequence 220, App
9	19	2.2	1196	4	US-09-149-476-225 Sequence 225, App
10	19	2.2	1220	4	US-09-149-476-57 Sequence 57, Appl
11	19	2.2	1514	4	US-09-213-768-1 Sequence 1, Appl
12	19	2.2	1539	4	US-09-668-680-13 Sequence 13, Appl
13	18	2.0	20	2	US-09-213-768-2 Sequence 2, Appl
14	18	2.0	2949	4	US-08-259-451-10 Sequence 10, Appl
15	18	2.0	3727	1	US-08-249-380-1 Sequence 1, Appl
16	18	2.0	8957	4	US-08-259-451-1 Sequence 1, Appl
17	17	1.9	44	4	US-09-182-145-152 Sequence 152, App
18	17	1.9	480	3	US-09-188-930-206 Sequence 206, App
19	17	1.9	614	4	US-08-998-416-151 Sequence 151, App
20	17	1.9	661	3	US-08-578-634C-3 Sequence 3, Appl
21	17	1.9	661	4	US-09-430-010-3 Sequence 3, Appl
22	17	1.9	896	3	US-09-188-930-36 Sequence 36, Appl
23	17	1.9	933	3	US-08-987-743-1 Sequence 1, Appl
24	17	1.9	1308	3	US-08-987-743-5 Sequence 5, Appl
25	17	1.9	1491	4	US-09-662-249A-3 Sequence 3, Appl
26	17	1.9	1743	3	US-08-665-259-20 Sequence 20, Appl
27	17	1.9	1743	3	US-08-762-500-20 Sequence 20, Appl

28	17	1.9	1821	4	US-09-149-476-90 Sequence 90, Appl
29	17	1.9	1974	3	US-08-762-500-78 Sequence 78, Appl
30	17	1.9	2517	3	US-08-733-360A-4 Sequence 4, Appl
31	17	1.9	2517	3	US-08-987-743-16 Sequence 16, Appl
32	17	1.9	2517	4	US-08-916-935-4 Sequence 4, Appl
33	17	1.9	3280	4	US-09-484-970B-43 Sequence 43, Appl
34	17	1.9	3865	4	US-09-149-476-296 Sequence 296, App
35	17	1.9	6803	3	US-08-665-259-19 Sequence 19, Appl
36	17	1.9	6803	3	US-08-762-500-19 Sequence 19, Appl
37	17	1.9	7874	4	US-09-780-175-96 Sequence 96, Appl
38	17	1.9	35828	4	US-09-449-218D-17 Sequence 17, Appl
39	17	1.9	81001	4	US-09-750-580-1 Sequence 1, Appl
40	17	1.9	111282	4	US-08-524-250-3 Sequence 3, Appl
41	16	1.8	31	1	US-08-524-250-3 Sequence 3, Appl
42	16	1.8	428	4	US-09-397-787-224 Sequence 224, App
43	16	1.8	435	4	US-09-397-787-280 Sequence 280, App
44	16	1.8	540	2	US-08-726-306A-182 Sequence 182, App
45	16	1.8	572	4	US-09-342-653-5 Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-09-182-145-17
; Sequence 17, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 17
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-182-145-17

Query Match      10.2%; Score 90; DB 4; Length 1734;
Best local Similarity 100.0%; Pred. No. 2.7e-34;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      410 AGTGTGTCACGAGGCTGGGGAGTCTTCGACCACTGTCATGTCGACCCAGCCA 469
      |||
Db      418 AGTGTGTCACGAGGCTGGGGAGTCTTCGACCACTGTCATGTCGACCCAGCCA 477
      |||

QY      470 GGGCCTGTTGTCAGCCTGGGGCAGGCC 499
      |||
Db      478 GGGCCTGTTGTCAGCCTGGGGCAGGCC 507
      |||

RESULT 2
US-09-182-145-18/c
; Sequence 18, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
```

```
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 18
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-182-145-18
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Query Match      10.2%; Score 90; DB 4; Length 1734;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      410 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACACCCAGCCA 469
          |||
Db       1317 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACACCCAGCCA 1258

QY      470 GGGCCTGTTGTCAGCCTGGGGCAGGCCC 499
          |||
Db       1257 GGGCCTGTTGTCAGCCTGGGGCAGGCCC 1228
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RESULT 3
US-09-182-145-38
; Sequence 38, Application US/09182145B
; Patent No. 6387657

GENERAL INFORMATION:

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; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 38
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-38
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Query Match 3.6%; Score 32; DB 4; Length 738;

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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      375 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 406
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Db       115 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 146
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RESULT 4
US-09-182-145-39

; Sequence 39, Application US/09182145B
; Patent No. 6387657

GENERAL INFORMATION:

```
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 39
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1-841
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-39
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Query Match 3.6%; Score 32; DB 4; Length 841;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      654 GAGATGTGCGGCTGCCAGCTGGGACTGCC 685
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Db       417 GAGATGTGCGGCTGCCAGCTGGGACTGCC 448
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RESULT 5
US-09-182-145-13

; Sequence 13, Application US/09182145B
; Patent No. 6387657

GENERAL INFORMATION:

```
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
```

```
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 13
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-13

Query Match          3.6%; Score 32; DB 4; Length 1293;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGATGGCTGTGCTGCTG 406
Db 148 GTACCCCTGTGCTGATGGCTGTGCTGCTG 179

RESULT 6
US-09-182-145-14/c
; Sequence 14, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 14
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-14

Query Match          3.6%; Score 32; DB 4; Length 1293;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGATGGCTGTGCTGCTG 406
Db 1146 GTACCCCTGTGCTGATGGCTGTGCTGCTG 1115

RESULT 7
US-09-182-145-117
; Sequence 117, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
```

```
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 117
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-51
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-117

Query Match          3.1%; Score 27; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 CCTGTGCTGATGGCTGTGCTGCTG 406
Db 1 CCTGTGCTGATGGCTGTGCTGCTG 27

RESULT 8
US-09-385-982-220/c
; Sequence 220, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 220
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(616)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-220

Query Match          2.2%; Score 19; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TGATGACGGTGGCTTCACC 635
Db 127 TGATGACGGTGGCTTCACC 109
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RESULT 9
US-09-149-476-225/C
; Sequence 225, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
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; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
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; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,313
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; EARLIER FILING DATE: 1997-10-02
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; Sequence 57, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; TITLE OF INVENTION: 186 Human Secreted proteins
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; CURRENT APPLICATION NUMBER: US/09/149,476
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; EARLIER FILING DATE: 1998-03-06
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

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Sequence 1, Application US/09213768
Patent No. 5985664
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
FILE REFERENCE: RTS-0026
CURRENT APPLICATION NUMBER: US/09/213,768
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(441)
US-09-213-768-1

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; Sequence 13, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_FL_genes Version 2.0
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; LOCATION: (130)..(1539)
US-09-668-680-13

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DB 774 CTTCCTCGCCTTCTCTCA 792

RESULT 13

US-09-213-768-2/c
; Sequence 2, Application US/09213768
; Patent No. 5985664
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2

; LENGTH: 20
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: PCR Primer
US-09-213-768-2

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; Sequence 10, Application US/08259451
; Patent No. 6406841
; GENERAL INFORMATION:
; APPLICANT: Lee, Helen H.
; APPLICANT: Swanson, Priscilla A.
; APPLICANT: Idler, Kenneth B.
; APPLICANT: Rosenblatt, Joseph D.
; APPLICANT: Chen, Irvin S. Y.
; APPLICANT: Golde, David W.
; APPLICANT: Robertson, Eugene F.
; APPLICANT: Stephens, John E.
; APPLICANT: Chan, Emerson W.
; APPLICANT: Buytendorp, Mark H.
; APPLICANT: Johnson, Joan E.
; APPLICANT: Motley, Cheryl T.
; APPLICANT: Peterson, Bryan
; APPLICANT: Edwards, Michelle
; APPLICANT: Guidinger, Peggy
; APPLICANT: Tate, Cynthia
; TITLE OF INVENTION: HTLV-IIINRA Compositions
; TITLE OF INVENTION: and Assays for Detecting HTLV Infection
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064

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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
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; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,415
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Daniel W. Collins
; REGISTRATION NUMBER: 31,912
; REFERENCE/DOCKET NUMBER: 5381.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-6365
; TELEFAX: (708) 938-2623
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear

US-08-259-451-10

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; Patent No. 5827685
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan
; TITLE OF INVENTION: Methods and Compositions of Genetic
; TITLE OF INVENTION: Stress Response Systems
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,380
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/710,187
; FILING DATE: 31-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
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; STRANDEDNESS: single
; TOPOLOGY: linear
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11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	883	100.0	1708	15	US-10-010-408-1 Sequence 1, Appl1
2	635	71.9	753	15	US-10-010-408-3 Sequence 3, Appl1
3	566	64.1	681	15	US-10-010-408-12 Sequence 12, Appl1
4	210	23.8	210	15	US-10-010-408-8 Sequence 8, Appl1
5	177	20.0	177	15	US-10-010-408-5 Sequence 5, Appl1
6	90	10.2	1734	15	US-10-112-267-17 Sequence 17, Appl1
7	90	10.2	1734	15	US-10-112-267-18 Sequence 18, Appl1
8	59	6.7	174	15	US-10-010-408-10 Sequence 10, Appl1
9	32	3.6	199	10	US-09-864-761-23432 Sequence 23432, A
10	32	3.6	586	10	US-09-864-761-6698 Sequence 6698, Ap
11	32	3.6	738	15	US-10-112-267-38 Sequence 38, Appl1
12	32	3.6	841	15	US-10-112-267-39 Sequence 39, Appl1
13	32	3.6	1266	14	US-10-137-866-319 Sequence 319, App
14	32	3.6	1266	14	US-10-146-726-319 Sequence 319, App
15	32	3.6	1266	14	US-10-146-727-319 Sequence 319, App
16	32	3.6	1266	14	US-10-146-788-319 Sequence 319, App

17	3.6	1266	14	US-10-152-380-319	Sequence 319, App
18	3.6	1266	15	US-10-153-934-319	Sequence 319, App
19	3.6	1266	15	US-10-028-072-319	Sequence 319, App
20	3.6	1266	15	US-10-121-049-319	Sequence 319, App
21	3.6	1266	15	US-10-123-904-319	Sequence 319, App
22	3.6	1266	15	US-10-140-470-319	Sequence 319, App
23	3.6	1266	15	US-10-175-746-319	Sequence 319, App
24	3.6	1266	15	US-10-176-918-319	Sequence 319, App
25	3.6	1266	15	US-10-176-921-319	Sequence 319, App
26	3.6	1266	15	US-10-137-865-319	Sequence 319, App
27	3.6	1266	15	US-10-140-474-319	Sequence 319, App
28	3.6	1266	15	US-10-142-431-319	Sequence 319, App
29	3.6	1266	15	US-10-143-114-319	Sequence 319, App
30	3.6	1266	15	US-10-140-002-319	Sequence 319, App
31	3.6	1266	15	US-10-142-419-319	Sequence 319, App
32	3.6	1266	15	US-10-123-262-319	Sequence 319, App
33	3.6	1266	15	US-10-142-423-319	Sequence 319, App
34	3.6	1266	15	US-10-121-050-319	Sequence 319, App
35	3.6	1266	15	US-10-141-755-319	Sequence 319, App
36	3.6	1266	15	US-10-143-032-319	Sequence 319, App
37	3.6	1266	15	US-10-123-108-319	Sequence 319, App
38	3.6	1266	15	US-10-123-236-319	Sequence 319, App
39	3.6	1266	15	US-10-123-261-319	Sequence 319, App
40	3.6	1266	15	US-10-140-921-319	Sequence 319, App
41	3.6	1266	15	US-10-140-928-319	Sequence 319, App
42	3.6	1266	15	US-10-121-045-319	Sequence 319, App
43	3.6	1266	15	US-10-123-292-319	Sequence 319, App
44	3.6	1266	15	US-10-123-903-319	Sequence 319, App
45	3.6	1266	15	US-10-124-819-319	Sequence 319, App

ALIGNMENTS

RESULT 1
US-10-010-408-1
; Sequence 1, Application US/10010408
; Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellet, Jr.
TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1708 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-010-408-1

Query Match 100.0%; Score 883; DB 15; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 883; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACGCTTCGATCTCCAGAGGACCCTGGGGTGGACAGGGCCCTGGCAAGGCTGCAGCC 60
Db 1 GACGCTTCGATCTCCAGAGGACCCTGGGGTGGACAGGGCCCTGGCAAGGCTGCAGCC 60
OY 61 GCTGGGAGTGGCTTGAATGAGGCTTTTATTACTGGAACTGAGAGCTAAGAGGCTC 120
Db 61 GCTGGGAGTGGCTTGAATGAGGCTTTTATTACTGGAACTGAGAGCTAAGAGGCTC 120
OY 121 CTGTACGCTTGTCTTAAAGCTTTAGACACTTGTGGCTTGGCTTACACACTGTGAGA 180
Db 121 CTGTACGCTTGTCTTAAAGCTTTAGACACTTGTGGCTTGGCTTACACACTGTGAGA 180
OY 181 CACCTTCGTGGCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAGGGAC 240
Db 181 CACCTTCGTGGCTCCACGGCCTCACCTTCAGGTTTGAAGCTGGCTCCACAGGGAC 240
OY 241 ACGGTGACATGAGGGGACGCCCACTGATCCATCTTCTGGCCACTTCCCTCTGCTTC 300
Db 241 ACGGTGACATGAGGGGACGCCCACTGATCCATCTTCTGGCCACTTCCCTCTGCTTC 300
OY 301 TCTCAATGCTGTGCCCCAGCTGTGCCGACACCTGTACTCTTCTTGACACCAACCC 360
Db 301 TCTCAATGCTGTGCCCCAGCTGTGCCGACACCTGTACTCTTCTTGACACCAACCC 360
OY 361 AGTCCCACAGGGGGTACCCCTGTGTGCTGATGCTGTGGCTGTAAAGTGTGAC 420
Db 361 AGTCCCACAGGGGGTACCCCTGTGTGCTGATGCTGTGGCTGTAAAGTGTGAC 420
OY 421 GGAGGCTGGGAGTCTCGACCACTGATGTCGACCCAGCCAGGCGCTGCTT 480
Db 421 GGAGGCTGGGAGTCTCGACCACTGATGTCGACCCAGCCAGGCGCTGCTT 480
OY 481 GTCAGCCTGGGGAGGCCCTGGCGCATGGGCTGTGTCTTGTGATGAGGATGACG 540
Db 481 GTCAGCCTGGGGAGGCCCTGGCGCATGGGCTGTGTCTTGTGATGAGGATGACG 540
OY 541 GTAGCTGTGAGTGAATGGCCGAGGTACCTGATGAGAGACCTTTAAACCAATTGCA 600
Db 541 GTAGCTGTGAGTGAATGGCCGAGGTACCTGATGAGAGACCTTTAAACCAATTGCA 600
OY 601 GGGTCTGTGCGCTGTGATGACGGTGGCTTCACTGCGCTGCTGTGAGTGAAGATG 660
Db 601 GGGTCTGTGCGCTGTGATGACGGTGGCTTCACTGCGCTGCTGTGAGTGAAGATG 660
OY 661 TGGGGTGGCCAGCTGGGACTGCCCCAGGCCCAAGAGATACAGGTGCCAGGAAGTCT 720
Db 661 TGGGGTGGCCAGCTGGGACTGCCCCAGGCCCAAGAGATACAGGTGCCAGGAAGTCT 720
OY 721 GCCCGAGTGGGTATGTGACAGGAGTGAACCGGCGATCCAGCGTCCACGGCGCAG 780
Db 721 GCCCGAGTGGGTATGTGACAGGAGTGAACCGGCGATCCAGCGTCCACGGCGCAG 780
OY 781 GACACCAACTTCTGCCCTGTGACTCTCTGCTGATGCTCTCTTGTCCAATTGGA 840
Db 781 GACACCAACTTCTGCCCTGTGACTCTCTGCTGATGCTCTCTTGTCCAATTGGA 840
OY 841 GCACAGCCTGGGGCCCCCTGCTCAACCACTGTGGGCTGGGCAT 883
Db 841 GCACAGCCTGGGGCCCCCTGCTCAACCACTGTGGGCTGGGCAT 883

Db 841 GCACAGCCTGGGGCCCCCTGCTCAACCACTGTGGGCTGGGCAT 883
RESULT 2
US-10-010-408-3
; Sequence 3, Application US/10010408
; Publication No. US20020165185A1
; GENERAL INFORMATION:
; APPLICANT: John J. Castellot, Jr.
; TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,408
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/044,273
; FILING DATE: March 19, 1998
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..750
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-010-408-3
Query Match 71.9%; Score 635; DB 15; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 249 ATGAGGGGACGCCCACTGATCCATCTTGGCCACTTCTCTCTGCTCTCTCAATG 308
Db 1 ATGAGGGGACGCCCACTGATCCATCTTGGCCACTTCTCTCTGCTCTCTCAATG 60
OY 309 GTGTGTGCCAGCTGTGCCGAGACACCCCTGATCTCTTGGACACACCCAGTGCCA 368
Db 61 GTGTGTGCCAGCTGTGCCGAGACACCCCTGATCTCTTGGACACACCCAGTGCCA 120
OY 369 CAGGGGTACCCCTGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGACAGGAGCTG 428
Db 121 CAGGGGTACCCCTGTGCTGGATGGCTGTGGCTGCTGTAAAGTGTGACAGGAGCTG 180
OY 429 GGGAGTCTCTGGAACCACTGATGTCTGGAACCCAGCCAGGCGCTGTTGTACGCT 488
Db 181 GGGAGTCTCTGGAACCACTGATGTCTGGAACCCAGCCAGGCGCTGTTGTACGCT 240


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: APPLICATION NUMBER: US/10/010,408
: FILING DATE: 07-Dec-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/044,273
: FILING DATE: March 19, 1998
: APPLICATION NUMBER: <Unknown>
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Amy E. Mandragouras
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: MBI-004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 210 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..210
: SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-010-408-8

Query Match      23.8%; Score 210; DB 15; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.9e-99;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      318 CAGCTGTGCCGACACCCTGTACCTGTCTCGACACCAACCCAGTGCACAGGGGTA 377
      |||||||
Db      1 CAGCTGTGCCGACACCCTGTACCTGTCTCGACACCAACCCAGTGCACAGGGGTA 60

QY      378 CCCCTGCTGTGATGGCTGTGCTGTCTGTAAGTGTGACACGAGAGGCTGGGGAGTCC 437
      |||||||
Db      61 CCCCTGCTGTGATGGCTGTGCTGTCTGTAAGTGTGACACGAGAGGCTGGGGAGTCC 120

QY      438 TGCACACACCTGCATGTCTGCGACACCCAGCCAGGGGCTGTTGTACGCTGGGGCAGGC 497
      |||||||
Db      121 TGCACACACCTGCATGTCTGCGACACCCAGCCAGGGGCTGTTGTACGCTGGGGCAGGC 180

QY      498 CCTGGCGGCATGGGGCTGTGTCTCTTG 527
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Db      181 CCTGGCGGCATGGGGCTGTGTCTCTTG 210

RESULT 5
US-10-010-408-5
: Sequence 5, Application US/10010408
: Publication No. US20020165185A1
: GENERAL INFORMATION:
: APPLICANT: John J. Castellot, Jr.
: TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
: and Uses Therefor
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/010,408
: FILING DATE: 07-Dec-2001

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: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/044,273
: FILING DATE: March 19, 1998
: APPLICATION NUMBER: <Unknown>
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Amy E. Mandragouras
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: MBI-004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 177 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..177
: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-408-5

Query Match          20.0%; Score 177; DB 15; Length 177;
Best Local Similarity 100.0%; Pred.No. 6.1e-82;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 TGTGAGGTGATGGCCGACAGGTACCTGATGAGAGACCTTTAAACCAATTGCAGGTC 605
      |||||||
Db 1 TGTGAGGTGATGGCCGACAGGTACCTGATGAGAGACCTTTAAACCAATTGCAGGTC 60

QY 606 CTGTGCCGCTGTGATGACGGGTGGCTTCACCTGCCCTGCCGCTGTGCAGTGAGGATGTGCCG 665
      |||||||
Db 61 CTGTGCCGCTGTGATGACGGGTGGCTTCACCTGCCCTGCCGCTGTGCAGTGAGGATGTGCCG 120

QY 666 CTGCCAGCTGGGACTGCCCAAGCCCCAAGAGAATACAGGTGCCAGGAAGTGCTGC 722
      |||||||
Db 121 CTGCCAGCTGGGACTGCCCAAGCCCCAAGAGAATACAGGTGCCAGGAAGTGCTGC 177

RESULT 6
US-10-112-267-17
: Sequence 17, Application US/10112267
: Publication No. US20030068678A1
: GENERAL INFORMATION:
: APPLICANT: Botstein, David A.
: APPLICANT: Cohen, Robert
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Lawrence, David A.
: APPLICANT: Levine, Arnold J.
: APPLICANT: Pennica, Diane
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: P1176R2
: CURRENT APPLICATION NUMBER: US/10/112,267
: CURRENT FILING DATE: 2002-03-27
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
: PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
: NUMBER OF SEQ ID NOS: 156
: SEQ ID NO 17
: LENGTH: 1734

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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-17

Query Match 10.2%; Score 90; DB 15; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCTGCATGTCTGCAGCCCA 469
|||||
Db 418 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCTGCATGTCTGCAGCCCA 477
OY 470 GGGCCTGTTGTGTCAGCCTGGGGCAGGCC 499
|||||
Db 478 GGGCCTGTTGTGTCAGCCTGGGGCAGGCC 507

RESULT 7

US-10-112-267-18/c
; Sequence 18, Application US/10112267
; Publication No. US20030068678A1

; GENERAL INFORMATION:

; APPLICANT: Bolstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 18
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-18

Query Match 10.2%; Score 90; DB 15; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCTGCATGTCTGCAGCCCA 469
|||||
Db 1317 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCTGCATGTCTGCAGCCCA 1258
OY 470 GGGCCTGTTGTGTCAGCCTGGGGCAGGCC 499
|||||
Db 1257 GGGCCTGTTGTGTCAGCCTGGGGCAGGCC 1228

RESULT 8

US-10-010-408-10
; Sequence 10, Application US/10010408
; Publication No. US20020165185A1

; GENERAL INFORMATION:

; APPLICANT: John J. Castelli, Jr.
; TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 174 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..174

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-408-10

Query Match 6.7%; Score 59; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 825 CCTGTCCAATTGGACACAGCCCTGGGGCCCTGCTCAACCACTGTGGCTGGCAT 883
|||||
Db 1 CCTGTCCAATTGGACACAGCCCTGGGGCCCTGCTCAACCACTGTGGCTGGCAT 59

RESULT 9

US-09-864-761-23432
; Sequence 23432, Application US/09864761
; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23432
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL139352.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: NT HIT: AF083500.1, EVALUATE 1.00e-108
; OTHER INFORMATION: SWISSPROT HIT: O19113, EVALUATE 9.00e-19
; US-09-864-761-23432
Query Match      3.6%; Score 32; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 654 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 685
|||||
Db 129 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 160

RESULT 10
US-09-864-761-6698
; Sequence 6698, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE END NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6698
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL139352.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; US-09-864-761-6698
Query Match      3.6%; Score 32; DB 10; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 654 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 685
|||||
Db 342 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 373

RESULT 11
US-10-112-267-38
; Sequence 38, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane

```
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 38
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-267-38
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```
Query Match          3.6%; Score 32; DB 15; Length 738;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 375 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 406
    |||||||
Db 115 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 146
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RESULT 12

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US-10-112-267-39
; Sequence 39, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 39
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-841
; OTHER INFORMATION: Sequence is synthesized.
US-10-112-267-39
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Query Match          3.6%; Score 32; DB 15; Length 841;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 654 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 685

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Db 417 GAGGATGTGGCGCTGCCAGCTGGGACTGCC 448
    |||||||
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RESULT 13

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US-10-137-866-319
; Sequence 319, Application US/10137866
; Publication No. US20030129689A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C151
; CURRENT APPLICATION NUMBER: US/10/137,866
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
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; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083545

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982

Query Match 3.6%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGATGCTGTGCTGCTG 406
|||||
Db 136 GTACCCCTGCTGATGCTGTGCTGCTG 167

RESULT 14
US-10-146-726-319
; Sequence 319, Application US/10146726


```
; Publication NO. US20030129690A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Tumas, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC308
; CURRENT APPLICATION NUMBER: US/10/146,726
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-146-726-319

Query Match      3.6%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GTACCCCTGTGCTGTGATGGCTGTGGCTGCTG 406
      |||||||||||||||||||||||||||||||||||
Db      136 GTACCCCTGTGCTGTGATGGCTGTGGCTGCTG 167

RESULT 15
US-10-146-727-319
; Sequence 319, Application US/10146727
; Publication No. US20030129691A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Tumas, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC312
; CURRENT APPLICATION NUMBER: US/10/146,727
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 319
; LENGTH: 1266
; TYPE: DNA
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```
; ORGANISM: Homo Sapien
; US-10-146-727-319

Query Match      3.6%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GTACCCCTGTGCTGTGATGGCTGTGGCTGCTG 406
      |||||||||||||||||||||||||||||||||||
Db      136 GTACCCCTGTGCTGTGATGGCTGTGGCTGCTG 167

Search completed: July 28, 2003, 15:36:31
Job time : 217.455 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:16:26 ; Search time 1566.4 Seconds
(without alignments)
9129.604 Million cell updates/sec

Title: US-10-010-408-1_COPY_1_883
Perfect score: 883
Sequence: 1 GACGCTTCGATCTCCAGAG.....ACCACCTGTGGCTGGGCAT 883

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inu:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	10.2	940	14 BQ937887	BQ937887 AGENCOURT
2	67	7.6	537	14 BQ560868	BQ560868 H4067A01-
3	49	5.5	424	10 BB849097	BB849097 BB849097
4	32	3.6	380	12 BG900020	BG900020 HOA48-1-G
5	32	3.6	405	12 BG900069	BG900069 HOA51-1-A
6	32	3.6	489	14 BM751866	BM751866 K-EST0028

7	32	3.6	618	12 BG538695	BG538695 602566932
8	32	3.6	620	13 BG928868	BG928868 HNC57-1-D
9	32	3.6	651	13 B1457141	B1457141 603185392
10	32	3.6	749	9 AL555144	AL555144 AL555144
11	32	3.6	750	13 BM043988	BM043988 603620978
12	32	3.6	790	13 BM046275	BM046275 603626068
13	32	3.6	800	13 B1826781	B1826781 603077268
14	32	3.6	886	13 B1822142	B1822142 603039845
15	32	3.6	888	13 B1825652	B1825652 603072631
16	32	3.6	916	13 B1457367	B1457367 603185689
17	32	3.6	928	13 B1161474	B1161474 602864871
18	32	3.6	933	14 BQ278961	BQ278961 AGENCOURT
19	32	3.6	979	14 BQ279131	BQ279131 AGENCOURT
20	32	3.6	1006	14 BM921531	BM921531 AGENCOURT
21	32	3.6	1022	14 BQ952960	BQ952960 AGENCOURT
22	32	3.6	1058	14 BM805088	BM805088 AGENCOURT
23	32	3.6	1073	14 BQ073722	BQ073722 AGENCOURT
24	32	3.6	1166	13 BM543799	BM543799 AGENCOURT
25	32	3.6	1251	14 BQ961357	BQ961357 AGENCOURT
26	30	3.4	190	9 AA647775	AA647775 vp04c09.r
27	23	2.6	436	17 AO095651	AO095651 HS_3017.A
28	23	2.6	742	13 B1758148	B1758148 603023866
29	23	2.6	792	13 B1823598	B1823598 603040962
30	23	2.6	966	12 BF141695	BF141695 601790752
31	21	2.4	495	13 B1204749	B1204749 EST522789
32	21	2.4	529	9 A1897896	A1897896 EST267339
33	21	2.4	561	12 BF051668	BF051668 EST436915
34	21	2.4	563	9 A1897344	A1897344 EST266787
35	21	2.4	609	9 A1485142	A1485142 EST243446
36	21	2.4	620	10 AW223381	AW223381 EST300192
37	20	2.3	188	14 H55466	H55466 CHR220405.C
38	20	2.3	232	9 AL658941	AL658941 AL658941
39	20	2.3	251	9 A1303895	A1303895 ui62f11.Y
40	20	2.3	288	10 BE574058	BE574058 IPBrn0148
41	20	2.3	319	13 BM389674	BM389674 UI-R-CN1-
42	20	2.3	332	17 AZ650040	AZ650040 1M0520D04
43	20	2.3	334	14 BM698298	BM698298 UI-E-DX0-
44	20	2.3	372	12 BF918366	BF918366 RC3-NT012
45	20	2.3	381	10 BE537338	BE537338 601064521

ALIGNMENTS

RESULT 1 BQ937887 940 bp mRNA linear EST 21-AUG-2002

LOCUS AGENCOURT_8951807 NCI_CGAP_CO24 Mus musculus cDNA clone

DEFINITION IMAGE:6476852 5', mRNA sequence.

ACCESSION BQ937887

VERSION BQ937887.1 GI:22353365

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 940)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM14017 row: n column: 21
High quality sequence stop: 543.
Location/Qualifiers

FEATURES
source 1. 940

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6476852"
/clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Colon; Vector: pGEM-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 169 a 277 c 288 g 200 t 6 others
ORIGIN

Query Match 10.2%; Score 90; DB 14; Length 940;
Best Local Similarity 100.0%; Pred. No. 9.6e-31;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGCACGAGGCTGGGGAGTCTCGCAGCAGGCGCATGTCTGCAGCCAGCCA 469
|||||
Db 444 AGTGTGCACGAGGCTGGGGAGTCTCGCAGCAGGCGCATGTCTGCAGCCAGCCA 503
QY 470 GGGCCTGTTGTACGCTGGGGCAGGCC 499
|||||
Db 504 GGGCCTGTTGTACGCTGGGGCAGGCC 533

RESULT 2 537 bp mRNA linear EST 20-JUN-2002
B0560868
LOCUS H4067A01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
DEFINITION H4067A01 5', mRNA sequence.
ACCESSION B0560868
VERSION B0560868.1 GI:21461753
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 537)
AUTHORS Vanburen,V., Plao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin
,P.R., Stagg,C.A., Bassey,U., Alba,K., Hamatani,T., Kargul,G.J.,
Luo,A.G. and Ko,M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set

JOURNAL Unpublished (2002)
COMMENT Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@ngs.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cdna/NIA_7_4k.html for details.
Plate: H4067 row: A column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 537
POLYA-No.

FEATURES

Source Location/Qualifiers

1..537
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="niaEST:H4067A01-5"
/db_xref="taxon:10090"
/clone="H4067A01"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

BASE COUNT 87 a 162 c 166 g 122 t
ORIGIN

Query Match 7.6%; Score 67; DB 14; Length 537;
Best Local Similarity 100.0%; Pred. No. 3.8e-20;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 410 AGTGTGCACGAGGCTGGGGAGTCTCGCAGCAGGCGCATGTCTGCAGCCAGCCA 469
|||||
Db 471 AGTGTGCACGAGGCTGGGGAGTCTCGCAGCAGGCGCATGTCTGCAGCCAGCCA 530
QY 470 GGGCCTG 476
|||||
Db 531 GGGCCTG 537

RESULT 3 424 bp mRNA linear EST 26-NOV-2001
BB849097
LOCUS BB849097 RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION BB849097 RIKEN full-length enriched, adult inner ear Mus musculus
cDNA clone F930006G02 5', mRNA sequence.
ACCESSION BB849097
VERSION BB849097.1 GI:17090551
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 424)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)

JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
Source Location/Qualifiers

1..424
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930006G02"
/clone_lib="RIKEN full-length enriched, adult inner ear"


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/tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues ; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=males), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed)"
embryo, sex=mixed"
BASE COUNT      65 a      124 c      132 g      103 t
ORIGIN

Query Match      5.5%; Score 49; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      410 AGTGTGTCACGAGCGCTGGGGAGTCTCCGACCACTGCATGCTGC 458
      |||||||||||||||||||||||||||||||||||||||||||
Db      373 AGTGTGTGCACGAGCGCTGGGGAGTCTCTCGACCACTGCATGCTGC 421

RESULT 4
BG900020      380 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HOA48-1-G2.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA
DEFINITION      , mRNA sequence.
ACCESSION      BG900020
VERSION      BG900020.1 GI:14310269
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 380)
AUTHORS      Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE      Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritis cartilage cDNA libraries
JOURNAL      Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE      21482651
COMMENT      Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
Source      Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      58 a      139 c      118 g      65 t
ORIGIN

Query Match      3.6%; Score 32; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GTACCCCTGTGCTGATGGCTGTGCTGCTG 406
      |||||||||||||||||||||||||||||||||||||||
Db      206 GTACCCCTGTGCTGATGGCTGTGCTGCTG 237

RESULT 5
BG900069
```

```
LOCUS      BG900069      405 bp      mRNA      linear      EST 06-NOV-2001
DEFINITION      HOA51-1-A11.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
cDNA, mRNA sequence.
ACCESSION      BG900069
VERSION      BG900069.1 GI:14310318
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 405)
AUTHORS      Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE      Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritis cartilage cDNA libraries
JOURNAL      Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE      21482651
COMMENT      Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
Source      Location/Qualifiers
1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      62 a      140 c      135 g      68 t
ORIGIN

Query Match      3.6%; Score 32; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GTACCCCTGTGCTGATGGCTGTGCTGCTG 406
      |||||||||||||||||||||||||||||||||||||||
Db      202 GTACCCCTGTGCTGATGGCTGTGCTGCTG 233

RESULT 6
BM751866      489 bp      mRNA      linear      EST 04-MAR-2002
LOCUS      K-EST0028180 S2SN0668s1 Homo sapiens cDNA clone S2SN0668s1-2-D09
DEFINITION      5', mRNA sequence.
ACCESSION      BM751866
VERSION      BM751866.1 GI:19081484
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 489)
AUTHORS      Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL      Unpublished (2002)
COMMENT      Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
```

Plate: 2 row: D column: 09
High quality sequence stop: 489.
Location/Qualifiers

FEATURES

source

1. 489

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S2SNU668s1-2-D09"
/clone_lib="S2SNU668s1"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-668"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was decapped with tobacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 15' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F with electroporation method."

BASE COUNT 75 a 173 c 159 g 82 t
ORIGIN

Query Match

Best Local Similarity 3.6%; Score 32; DB 14; Length 489;
Matches 32; Conservativity 100.0%; Pred. No. 0.0006;

Indels 0; Gaps 0;

OY 654 GAGGATGTGCGCTGCCAGCTGGAGCTGCC 685

Db 139 GAGGATGTGCGCTGCCAGCTGGAGCTGCC 170

RESULT 7
BG538695
LOCUS

DEFINITION 618 bp mRNA linear EST 03-APR-2001
602566932F1 NIH_MGC_77 Homo sapiens cDNA, clone IMAGE:4691574 5',
mRNA sequence.

ACCESSION BG538695

VERSION BG538695.1 GI:13530928

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 618)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1510 row: p column: 07
High quality sequence stop: 499.
Location/Qualifiers

FEATURES

source

1. 618

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4691574"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccatcgcc); Site_2: SfiI (ggccatcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."

BASE COUNT 95 a 194 c 213 g 116 t
ORIGIN

Query Match

Best Local Similarity 3.6%; Score 32; DB 12; Length 618;
Matches 32; Conservativity 100.0%; Pred. No. 0.00063;

Indels 0; Gaps 0;

OY 375 GTACCCCTGTGCTGATGCTGTGCTGTG 406

Db 291 GTACCCCTGTGCTGATGCTGTGCTGTG 322

RESULT 8
BG928868
LOCUS

DEFINITION 620 bp mRNA linear EST 06-NOV-2001
HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BG928868

VERSION BG928868.1 GI:14323391

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 620)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.

TITLE

Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and

osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL

MEDLINE

COMMENT

CONTACT: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay_kumar-1@sk.com

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Seq primer: T7.

Query Match 3.6%; Score 32; DB 13; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 210 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 241

RESULT 9
BI457141 651 bp mRNA linear EST 21-AUG-2001
LOCUS 603185392F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258159 5',
DEFINITION mRNA sequence.
ACCESSION BI457141
VERSION BI457141 GI:15247797
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 651)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LICM1869 row: g column: 24
High quality sequence stop: 651.

FEATURES
Source
1. 651
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258159"
/clone_1ib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. |"

BASE COUNT 91 a 230 c 219 g 111 t
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 651;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 96 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 127

RESULT 10
AL555144 749 bp mRNA linear EST 16-FEB-2001
LOCUS AL555144 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK007YO21 5
DEFINITION prime, mRNA sequence.
ACCESSION AL555144
VERSION AL555144 GI:12896595

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 749)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
1. 749
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DK007YO21"
/clone_1ib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 128 a 252 c 236 g 133 t
ORIGIN

Query Match 3.6%; Score 32; DB 9; Length 749;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 406
|||||
Db 432 GTACCCCTGCTGCTGATGCGCTGTGGCTGCTG 463

RESULT 11
BM043988 750 bp mRNA linear EST 07-NOV-2001
LOCUS BM043988
DEFINITION 603620978F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5446794 5',
mRNA sequence.
ACCESSION BM043988
VERSION BM043988.1 GI:16773255
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 750)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LICM1929 row: k column: 19
High quality sequence stop: 714.

FEATURES
Source
1. 750
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IMAGE:5446794"
/clone_1lb="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 112 a 267 c 246 g 125 t
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGATGCTGTGGCTGCTG 406
Db 142 GTACCCCTGTGCTGATGCTGTGGCTGCTG 173

RESULT 12
BM046275 790 bp mRNA linear EST 07-NOV-2001
LOCUS 603626068F1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5452480 5',
DEFINITION mRNA sequence.
ACCESSION BM046275 GI:16775542
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1944 row: h column: 17
High quality sequence stop: 780.

FEATURES
source
Location/Qualifiers
1..790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5452480"
/clone_1lb="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 121 a 265 c 269 g 135 t
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 790;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GAGATGTGCGGCTGCCAGCTGGAGTGGCC 685
Db 265 GAGATGTGCGGCTGCCAGCTGGAGTGGCC 296

RESULT 13
BI826781 800 bp mRNA linear EST 04-OCT-2001
LOCUS 603077268F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5180650 5',
DEFINITION mRNA sequence.
ACCESSION BI826781 GI:15938331
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11420 row: g column: 18
High quality sequence stop: 788.

FEATURES
source
Location/Qualifiers
1..800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5180650"
/clone_1lb="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

BASE COUNT 115 a 284 c 264 g 136 t 1 others
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 800;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GTACCCCTGTGCTGATGCTGTGGCTGCTG 406
Db 120 GTACCCCTGTGCTGATGCTGTGGCTGCTG 151

RESULT 14
BI822142 886 bp mRNA linear EST 04-OCT-2001
LOCUS 603039845F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5180650 5',
DEFINITION mRNA sequence.
ACCESSION BI822142 GI:15933692
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11450 row: j column: 11
High quality sequence stop: 865.

Location/Qualifiers
1. .886

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5180650"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 134 a 310 c 288 g 154 t
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 406
|||||
Db 121 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 152

RESULT 15
BI825652 888 bp mRNA linear EST 04-OCT-2001
LOCUS 603072631F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5164614 5',
DEFINITION mRNA sequence.
ACCESSION BI825652
VERSION BI825652.1 GI:15937202
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 888)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11408 row: n column: 07
High quality sequence stop: 877.
Location/Qualifiers

source 1. .888
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5164614"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
BASE COUNT 130 a 308 c 288 g 162 t
ORIGIN

Query Match 3.6%; Score 32; DB 13; Length 888;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 406
|||||
Db 117 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 148

Search completed: July 28, 2003, 18:02:04
Job time : 1568.4 secs

FEATURES

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:19:16 ; Search time 2092.59 Seconds

(without alignments)
10472.371 Million cell updates/sec

Title: US-10-010-408-3

Perfect score: 753
Sequence: 1 ATGAGGGGACGCCACTGAT.....CATGACAGTGCTTCTAA 753

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	31.2	1741	10 AF259981	AF259981 Rattus no
2	223	29.6	137964	2 AC126895	AC126895 Rattus no
3	223	29.6	226303	2 AC095418	AC095418 Rattus no
4	154	20.5	137964	2 AC126895	AC126895 Rattus no
5	90	12.0	1734	6 AR210324	AR210324 Sequence
6	90	12.0	1734	6 AR210325	AR210325 Sequence
7	90	12.0	1734	10 AF100778	AF100778 Mus muscu
8	90	12.0	61072	10 AL731698	AL731698 Mouse DNA
9	90	12.0	216757	2 AL669906	AL669906 Mus muscu
10	80	10.6	1739	10 AF126063	AF126063 Mus muscu
11	32	4.2	738	6 AR210337	AR210337 Sequence
12	32	4.2	841	6 AR210338	AR210338 Sequence
13	32	4.2	1266	6 AX076919	AX076919 Sequence
14	32	4.2	1266	6 AX464186	AX464186 Sequence
15	32	4.2	1283	9 AF083500	AF083500 Homo sapi
16	32	4.2	1293	6 AR210322	AR210322 Sequence
17	32	4.2	1293	6 AR210323	AR210323 Sequence
18	32	4.2	1309	9 AF074604	AF074604 Homo sapi
19	32	4.2	1427	9 AF100780	AF100780 Homo sapi
20	32	4.2	1450	9 BC017782	BC017782 Homo sapi
21	32	4.2	107260	9 AL139352	AL139352 Human DNA
22	27	3.6	51	6 AR210371	AR210371 Sequence
23	27	3.6	51	6 AX076923	AX076923 Sequence
24	22	2.9	99395	2 AC010446	AC010446 Homo sapi
25	22	2.9	149483	2 AC110904	AC110904 Mus muscu
26	22	2.9	180464	2 AC116351	AC116351 Homo sapi
27	22	2.9	200050	1 AL646068	AL646068 Ralstonia
28	21	2.8	66908	2 AC119914	AC119914 Mus muscu
29	21	2.8	150944	2 AC112856	AC112856 Rattus no
30	21	2.8	181343	10 AL671882	AL671882 Mouse DNA
31	21	2.8	204937	2 AL831741	AL831741 Mus muscu
32	21	2.8	215105	2 AC073717	AC073717 Mus muscu
33	20	2.7	1003	5 CHKTCBA	M73064 Chicken T-c
34	20	2.7	1200	6 AX122384	AX122384 Sequence
35	20	2.7	1221	9 HSM801506	AL133637 Homo sapi
36	20	2.7	1481	8 AB033535	AB033535 Oryza sat
37	20	2.7	3301	9 BC019257	BC019257 Homo sapi
38	20	2.7	4467	9 AB020659	AB020659 Homo sapi
39	20	2.7	7172	10 AB008516	AB008516 Mus muscu
40	20	2.7	36296	9 HSE81G9	Z82180 Human DNA s
41	20	2.7	83021	2 AC095541	AC095541 Rattus no
42	20	2.7	84001	9 AL162739	AL162739 Human DNA
43	20	2.7	92458	9 AL353715	AL353715 Human DNA
44	20	2.7	114793	9 AF217796	AF217796 Homo sapi
45	20	2.7	117840	9 AL162400	AL162400 Human DNA

ALIGNMENTS

RESULT 1
AF259981
LOCUS 1741 bp mRNA linear ROD 09-MAY-2000
DEFINITION Rattus norvegicus CCN family protein COP-1 (COP-1) mRNA, complete
cds.
ACCESSION AF259981
VERSION AF259981.1 GI:7739780
KEYWORDS
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1741)
AUTHORS Zhang, R., Averboukh, L., Zhu, W., Zhang, H., Jo, H., Dempsey, P.J.,

TITLE	JOURNAL	DATE
Coffey, R.J., Pardee, A.B. and Liang, P. Identification of rCop-1, a new member of the CCN protein family, as a negative regulator for cell transformation	MOL. CELL. BIOL. 18 (10), 6131-6141 (1998)	1998

JOURNAL. CELL. BIOL. 18 (10), 6131-6141 (1998)
MEDLINE 98414629

PUBMED 9742130

REFERENCE 2 (bases 1 to 1741)

AUTHORS Liang, P.

TITLE Direct Submission
JOURNAL Submitted (24-APR-2000) Cell Biology, Vanderbilt-Ingram Cancer

Center, 649 MRB II, Nashville, TN 37232, USA

FEATURES

location/qualifiers

Source

/organism- "Rattus norvegicus"

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/db_xref="taxon:10116"
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gene

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/gene="Cop-1"
262. .1014
CDS

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/gene="Cop-1"

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/note="secreted protein"
/codon_start=1

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/product="CCN family protein COP-1"
/protein_id="AAFG9011.1"

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/db_xref="GI:7739781"

/translation-"MRGSPILRLATSFLCLLSMVC AOLCRTPCTCPWTPPOCPQGV

LVL D G C G C C K V C A R R L T E S C E H L H V C E P S G G L V C Q P G A G P G G H G A V C L L D E D D G D C E V

NGRRYLDGETFKPNCRVLCRCDDGGFTCLPLGSEDTVTLPSWDCPRPKRIOVPGKCCE

WVCDQGVTPAIQRSAQGHQLSALVTPASADAIF
ONRFOLEIOBRCLPRPCLARSHSSWSNAF"

BASE COUNT	a	c	d	f
386	491	480	384	

ORIGIN

Query Match

Best Local Similarity 99.48; Pred. No. 1.6e-116;

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Matches 335; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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417 GCTGCCAGCTGGACTGCCACGCCCAAGAGATACAGGTGCCAGGAAGTGTGCC 476

157

4 / CGAGTGGGTATGTGACCGAGTGGGATCCAGTCTCCACGGCCGCAAGGACAC

DD /38 CGAGTGGGTAATGTGACCCAGGGAGTGTACACCCGGCGGATCCAGCGCTCCGGGGCCAGGACA /9/

[illegible][illegible][illegible][illegible]

Db 858 AGCCTGGGGCCCTGCTCAACCACTGTGGGCTGGGCATAGCCACCAGTGTCCAACCA

657 GAACGATTCTGCCACTGGAGATCCAACGCCCGCTGTGTCTGCCAGACCTGCCTGCC 716

THE UNIVERSITY OF CHICAGO

REFERENCE	TITLE	REFERENCE	TITLE
1 (bases 1 to 137964)	Rattus.	1 (bases 1 to 137964)	Rattus.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alshrocks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J., Benton,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homs,i.F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., Mcleod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogunh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Qulles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.			
2 (bases 1 to 137964)	Unpublished	2 (bases 1 to 137964)	Unpublished
Worley,K.C.	Direct Submission	Worley,K.C.	Direct Submission
Submitted (10-JUL-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (10-JUL-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 137964)	Worley,K.C.	3 (bases 1 to 137964)	Worley,K.C.
Direct Submission	Submitted (24-JUL-2002)	Direct Submission	Submitted (24-JUL-2002)
Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Genome Center	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Genome Center

Eukaryota; metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 49 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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* 15752 17494: contig of 1743 bp in length
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* 17595 18679: contig of 1085 bp in length
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* 57583 60781: contig of 3199 bp in length
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* 70940 75139: contig of 4200 bp in length
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* 107081 107180: gap of unknown length
* 107181 115201: contig of 8021 bp in length
* 115202 115301: gap of unknown length
* 115302 121237: contig of 5936 bp in length
* 121238 121337: gap of unknown length
* 121338 127910: contig of 6573 bp in length
* 127911 128010: gap of unknown length
* 128011 137964: contig of 9954 bp in length.
* location/Qualifiers
* 1. 137964
* /organism="Rattus norvegicus"
* /db_xref="taxon:10116"
* /clone="CH230-301E4"

BASE COUNT 31831 a 34027 c 35229 g 31979 t 4898 others
ORIGIN

Query Match 29.6%; Score 223; DB 2; Length 137964;
Best Local Similarity 100.0%; Pred. No. 3.1e-110;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 531 AGGACACCACTTCTGCCCCCTGTGCTCAACCACTGTGGGCTGGCATAGCCAGAGTGTG 590
|||||
Db 44065 AGGACACCACTTCTGCCCTGTGCTCAACCACTGTGGGCTGGCATAGCCAGAGTGTG 44124
OY 591 GAGCACAGCCTGGGGCCCCCTGTGCTCAACCACTGTGGGCTGGCATAGCCAGAGTGTG 650
|||||
Db 44125 GAGCACAGCCTGGGGCCCCCTGTGCTCAACCACTGTGGGCTGGCATAGCCAGAGTGTG 44184
OY 651 CAACCAAGACCGATTCTGCGCACTGAGATCCACGCCGCGCTGTGTGCCAGACCCTG 710
|||||
Db 44185 CAACCAAGACCGATTCTGCGCACTGAGATCCACGCCGCGCTGTGTGCCAGACCCTG 44244
OY 711 CCTGGCAGCCAGAGCCACACAGCTCATGTGAGACAGTGTCTTAA 753
|||||
Db 44245 CCTGGCAGCCAGAGCCACACAGCTCATGTGAGACAGTGTCTTAA 44287

RESULT 3
AC095418 226303 bp DNA linear HTG 11-JUL-2002
LOCUS AC095418 Rattus norvegicus clone CH230-7C10, *** SEQUENCING IN PROGRESS ***
DEFINITION 51 unordered pieces.
ACCESSION AC095418
VERSION AC095418.3 GI:21717893
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 226303)
Muzny,D.M., Adams,C., Adio-Oduola,B., Allsoman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbala,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 226303)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 226303)
Worley,K.C.
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17941885.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCDF
Center clone name: CH230-7C10
----- Summary Statistics
Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 185950 bases at least Q40
Consensus quality: 190362 bases at least Q30
Consensus quality: 193076 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 51 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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* 180491 191272: contig of 10782 bp in length
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FEATURES
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/db_xref="taxon:10116"
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BASE COUNT 57875 a 53353 c 52917 g 57041 t 5117 others

Query Match 29.6% Score 223; DB 2; Length 226303;
Best Local Similarity 100.0% Pred. No. 2.9e-110;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4 AC126895/c 137964 bp DNA linear HTG 24-JUL-2002
LOCUS Rattus norvegicus clone CH230-301E4, *** SEQUENCING IN PROGRESS
DEFINITION *** 49 unordered pieces.
ACCESSION AC126895

VERSION AC126895.1 GI:21724040
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SOURCE Rattus norvegicus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.

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Muzny,D.M., Adams,C., Adio-Oduola,B., All-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oyiedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Qulles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaikie,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and gibbs,R.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 137964)
Worley,K.C.
AUTHORS Direct Submission
TITTLE Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 137964)
Worley,K.C.
AUTHORS Direct Submission
TITTLE Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
JOURNAL of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project information
Center project name: GZHG
Center clone name: CH230-301E4
Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329
Consensus quality: 89474 bases at least Q40
Consensus quality: 93422 bases at least Q30
Consensus quality: 96506 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 49 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1056: contig of 1056 bp in length
1057 1156: gap of unknown length
1157 2335: contig of 1179 bp in length
2335 2435: gap of unknown length
2435 3442: contig of 1007 bp in length
3442 3542: gap of unknown length
3542 5081: contig of 1539 bp in length
5081 5181: gap of unknown length
5181 6424: contig of 1243 bp in length
6424 6524: gap of unknown length
6524 7814: contig of 1290 bp in length
7814 7914: gap of unknown length
7914 9153: contig of 1239 bp in length
9153 9253: gap of unknown length
9253 10445: contig of 1192 bp in length
10445 10545: gap of unknown length
10545 11771: contig of 1226 bp in length
11771 11871: gap of unknown length
11871 13240: contig of 1369 bp in length
13240 13340: gap of unknown length
13340 14359: contig of 1019 bp in length
14359 14459: gap of unknown length
14459 15651: contig of 1192 bp in length
15651 15751: gap of unknown length
15751 17494: contig of 1743 bp in length
17494 17594: gap of unknown length
17594 18679: contig of 1085 bp in length
18679 20681: contig of 1902 bp in length
20681 20781: gap of unknown length
20781 22118: contig of 1337 bp in length
22118 22218: gap of unknown length
22218 23578: contig of 1360 bp in length
23578 23678: gap of unknown length
23678 25423: contig of 1745 bp in length
25423 25523: gap of unknown length
25523 27808: contig of 2285 bp in length
27808 27908: gap of unknown length
27908 30272: contig of 2364 bp in length
30272 30372: gap of unknown length
30372 33091: contig of 2719 bp in length
33091 33191: gap of unknown length
33191 35777: contig of 2586 bp in length
35777 35877: gap of unknown length
35877 36908: contig of 1031 bp in length
36908 37008: gap of unknown length
37008 38930: contig of 1922 bp in length
38930 39030: gap of unknown length
39030 41210: contig of 2180 bp in length
41210 41310: gap of unknown length
41310 42937: contig of 1627 bp in length
42937 43037: gap of unknown length
43037 46120: contig of 3083 bp in length
46120 46220: gap of unknown length
46220 48217: contig of 1997 bp in length
48217 48317: gap of unknown length
48317 50433: contig of 2116 bp in length
50433 50533: gap of unknown length

50534 52880: contig of 2347 bp in length
52880 52980: gap of unknown length
52980 55194: contig of 2214 bp in length
55194 55294: gap of unknown length
55294 57482: contig of 2188 bp in length
57482 57582: gap of unknown length
57582 60781: contig of 3199 bp in length
60781 60881: gap of unknown length
60881 62599: contig of 1718 bp in length
62599 62600: gap of unknown length
62600 65200: contig of 2504 bp in length
65200 65204: gap of unknown length
65204 66914: contig of 1611 bp in length
66914 67014: gap of unknown length
67014 70839: contig of 3825 bp in length
70839 70939: gap of unknown length
70939 75139: contig of 4200 bp in length
75139 75239: gap of unknown length
75239 78296: contig of 3057 bp in length
78296 78396: gap of unknown length
78396 83138: contig of 4742 bp in length
83138 83238: gap of unknown length
83238 88204: contig of 4966 bp in length
88204 88304: gap of unknown length
88304 92238: contig of 3934 bp in length
92238 92338: gap of unknown length
92338 97339: contig of 5001 bp in length
97339 97439: gap of unknown length
97439 103534: contig of 6095 bp in length
103534 103635: gap of unknown length
103635 107080: contig of 3446 bp in length
107080 107180: gap of unknown length
107180 115201: contig of 8021 bp in length
115201 115301: gap of unknown length
115301 121237: contig of 5936 bp in length
121237 121337: gap of unknown length
121337 127910: contig of 6573 bp in length
127910 128010: gap of unknown length
128010 137964: contig of 9954 bp in length.
128011 137964: contig of 9954 bp in length.

FEATURES
Source 1. 137964
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-301E4"

BASE COUNT 31831 a 34027 c 35229 g 31979 t 4898 others
ORIGIN

Query Match 20.5%; Score 154; DB 2; Length 137964;
Best Local Similarity 100.0%; Pred. No. 1.3e-72;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TGGATGAGATGACGGGTAGCTGTGAGGTGAATGGCCGACAGGTACTGATGGAGAGACCT 337
|||||
Db 77246 TGGATGAGATGACGGGTAGCTGTGAGGTGAATGGCCGACAGGTACTGATGGAGAGACCT 77187

QY 338 TTAACCCCAATTGCAGGGTCTGTGCCGCTGTGATGACGGGTGCTTCACTGCTGCCGC 397
|||||
Db 77186 TTAACCCCAATTGCAGGGTCTGTGCCGCTGTGATGACGGGTGCTTCACTGCTGCCGC 77127

QY 398 TGTGAGTGAAGATGTGCGGCTGCCACCTGGGA 431
|||||
Db 77126 TGTGAGTGAAGATGTGCGGCTGCCACCTGGGA 77093

RESULT 5
AR210324 1734 bp DNA linear PAT 20-JUN-2002
LOCUS AR210324
DEFINITION Sequence 17 from patent US 6387657.
ACCESSION AR210324
VERSION AR210324.1 GI:21512525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE Unclassified.
1 (bases 1 to 1734)
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 17 14-MAY-2002;
FEATURES Location/Qualifiers
source 1. 1734
BASE COUNT 355 a 491 c 495 g 393 t
ORIGIN

Query Match 12.0%; Score 90; DB 6; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACCCAGCCA 221
Db 418 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACCCAGCCA 477

QY 222 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 251
Db 478 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 507

RESULT 6
AR210325/c AR210325 1734 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 18 from patent US 6387657.
DEFINITION AR210325
ACCESSION AR210325
VERSION AR210325.1 GI:21512526
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1734)
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 18 14-MAY-2002;
FEATURES Location/Qualifiers
source 1. 1734
BASE COUNT 393 a 495 c 491 g 355 t
ORIGIN

Query Match 12.0%; Score 90; DB 6; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACCCAGCCA 221
Db 1317 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACCCAGCCA 1258

QY 222 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 251
Db 1257 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 1228

RESULT 7
AF100778 1734 bp mRNA linear ROD 17-DEC-1998
LOCUS AF100778
DEFINITION Mus musculus connective tissue growth factor related protein WISP-2
(WISP2) mRNA, complete cds.
ACCESSION AF100778
VERSION AF100778
KEYWORDS AF100778.1 GI:4028578
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1734)
AUTHORS Pennica,D., Swanson,T.A., Welsh,J.W., Roy,M.A., Lawrence,D.A.,

JOURNAL Lee,J., Brush,J., Taneyhill,E.A., Deuel,B., Lew,M., Watanabe,C.,
Cohen,R.L., Melhem,M.F., Finley,G.G., Quirke,P., Goddard,A.D.,
Hillan,K.J., Gurney,A.L., Botstein,D. and Levine,A.J.
TITLE WISP genes are members of the connective tissue growth factor
family that are up-regulated in wnt-1-transformed cells and
aberrantly expressed in human colon tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14717-14722 (1998)
MEDLINE 99061933
PUBMED 9843955
REFERENCE 2 (bases 1 to 1734)
AUTHORS Pennica,D.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1998) Molecular Oncology, Genentech, Inc., 1 DNA
Way, South San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
source 1. 1734
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="C57MG"
/cell_type="epithelial"
/tissue_type="mammary"
/note="transformed by Wnt-1"
1. 1734
/gene="Wisp2"
257. 1012
/gene="Wisp2"
/codon_start=1
/product="connective tissue growth factor related protein
WISP-2"
/protein_id="AAC96320.1"
/db_xref="GI:4028579"
/translation="MRGNPLHLIAISFLCILSMVYSOLCPAPACAPWTPQCPGVP
LVLDGCGCCRVCARLIGESCDHLVCDPSQGLVCPGAPSGRGAVCLFEEDGCEV
NGRRYLDGETFKPNCRVLCRDDGGFTCLPLCSEDEVRLPSWDCPRPRIRIQVRCRPE
WVCDQAVMQPAIQPSASQGHQLSLVTPASADGPCPWNSTAWGPCSTTCGLGITRVS
NONRFOLEIQRRLCLSRPCLASRSHGWSNAF"

QY 162 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACCCAGCCA 221
Db 418 AGTGTGTCACGAGGCTGGGGAGTCTCGACACCACTGCATGTCGACCCAGCCA 477

QY 222 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 251
Db 478 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 507

RESULT 8
AL731698 61072 bp DNA linear ROD 24-MAY-2002
LOCUS AL731698
DEFINITION Mouse DNA sequence from clone RP23-161B3 on chromosome 2, complete
sequence.
ACCESSION AL731698
VERSION AL731698.10 GI:21214309
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 61072)
AUTHORS Wallis,J.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:21213601.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-161B3 is from the RPCI-23 Mouse PAC Library.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

FEATURES

source

location/Qualifiers

1. 61072

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="2"

/clone_1lb="RPCI-23"

/clone_1lb="RPCI-23"

BASE COUNT 15405 a 15368 c 15033 g 15266 t

ORIGIN

Query Match

12.0%; Score 90; DB 10; Length 61072;

Best Local Similarity 100.0%; Pred. No. 1.1e-37;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTCACGAGGCTGGGGAGTCTGCGACCACTGCATGCTGCGACCCAGCCA 221

DB 10029 AGTGTGTCACGAGGCTGGGGAGTCTGCGACCACTGCATGCTGCGACCCAGCCA 10088

QY 222 GGGCGTGTTCACAGCTGGGGCAGGCC 251

DB 10089 GGGCGTGTTCACAGCTGGGGCAGGCC 10118

RESULT 9

AL669906

LOCUS

DEFINITION AL669906 216757 bp DNA 1linear HTG 24-JUL-2002

MUS musculus chromosome 2 clone RP23-217C2, *** SEQUENCING IN

PROGRESS *** 21 unordered pieces.

ACCESSION AL669906

VERSION AL669906.5 GI:21955520

KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.

SOURCE Mus musculus.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 216757)

Sims, S.

Direct Submission

Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

On Jul 25, 2002 this sequence version replaced gi:18181793.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bm217C2

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 211865 bases at least Q40

Consensus quality: 213403 bases at least Q30
Consensus quality: 214139 bases at least Q20
Insert size: 214757; sum-of-contigs
Insert size: 234243; 1.8% error; agarose-fp
Quality coverage: 6.29x in Q20 bases; sum-of-contigs Quality
coverage: 5.90x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 4000: contig of 4000 bp in length
* 4001 4100: gap of 100 bp
* 4101 15267: contig of 11167 bp in length
* 15268 15367: gap of 100 bp
* 15368 34970: contig of 19603 bp in length
* 34971 35070: gap of 100 bp
* 35071 39671: contig of 4601 bp in length
* 39672 39771: gap of 100 bp
* 39772 46360: contig of 6589 bp in length
* 46361 46460: gap of 100 bp
* 46461 49809: contig of 3349 bp in length
* 49810 49909: gap of 100 bp
* 49910 54509: contig of 4600 bp in length
* 54510 54609: gap of 100 bp
* 54610 65989: contig of 11380 bp in length
* 65990 66089: gap of 100 bp
* 66090 84635: contig of 18546 bp in length
* 84636 84735: gap of 100 bp
* 84736 87399: contig of 2664 bp in length
* 87400 87499: gap of 100 bp
* 87500 98601: contig of 11102 bp in length
* 98602 98701: gap of 100 bp
* 98702 105522: contig of 6821 bp in length
* 105523 105622: gap of 100 bp
* 105623 119773: contig of 14151 bp in length
* 119774 119873: gap of 100 bp
* 119874 134552: contig of 14679 bp in length
* 134553 134652: gap of 100 bp
* 134653 141202: contig of 6550 bp in length
* 141203 141302: gap of 100 bp
* 141303 145808: contig of 4506 bp in length
* 145809 145908: gap of 100 bp
* 145909 151572: contig of 5664 bp in length
* 151573 151672: gap of 100 bp
* 151673 169686: contig of 18014 bp in length
* 169687 169786: gap of 100 bp
* 169787 200095: contig of 30309 bp in length
* 200096 200195: gap of 100 bp
* 200196 213877: contig of 13682 bp in length
* 213878 213977: gap of 100 bp
* 213978 216757: contig of 2780 bp in length.

FEATURES

source

location/Qualifiers

1. 216757

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="2"

/clone="RP23-217C2"

/clone_1lb="RPCI-23"

1. 4000

/note="assembly_fragment:03429

clone_end:SP6

vector_side:left"

4101. 15267

/note="assembly_fragment:00814

fragment_chain:1"

15368. 34970

/note="assembly_fragment:00812

fragment_chain:1"

misc_feature	35071..39671	/note="assembly_fragment:03544 fragment_chain:1"
misc_feature	39772..46360	/note="assembly_fragment:01438 fragment_chain:1"
misc_feature	46461..49809	/note="assembly_fragment:03410 fragment_chain:2"
misc_feature	49910..54509	/note="assembly_fragment:00811 fragment_chain:2"
misc_feature	54610..65989	/note="assembly_fragment:02217 fragment_chain:2"
misc_feature	66090..84635	/note="assembly_fragment:03529 fragment_chain:2"
misc_feature	84736..87399	/note="assembly_fragment:01019 fragment_chain:3"
misc_feature	87500..98601	/note="assembly_fragment:01170 fragment_chain:3"
misc_feature	98702..105522	/note="assembly_fragment:02829 fragment_chain:3"
misc_feature	105623..119773	/note="assembly_fragment:01476 fragment_chain:4"
misc_feature	119874..134552	/note="assembly_fragment:00505 fragment_chain:4"
misc_feature	134653..141202	/note="assembly_fragment:01951 fragment_chain:4"
misc_feature	141303..145808	/note="assembly_fragment:02637 fragment_chain:5"
misc_feature	145909..151572	/note="assembly_fragment:02352 fragment_chain:5"
misc_feature	151673..169686	/note="assembly_fragment:02207 fragment_chain:5"
misc_feature	169787..200095	/note="assembly_fragment:02849 fragment_chain:6"
misc_feature	200196..213877	/note="assembly_fragment:01052 fragment_chain:6"
misc_feature	213978..216757	/note="assembly_fragment:01318 clone_end:T7 vector_side:right"
BASE COUNT 56425 a 51573 c 51904 g 54852 t 2003 others		
ORIGIN		

Query Match 12.0%; Score 90; DB 2; Length 216757;		
Best Local Similarity 100.0%; Pred. No. 9.5e-38;		
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	162	AGTGTGTGCACGAGGCTGGGGAGTCTCGGACACCTGCATGTCGACCCAGCCA 221
Db	166450	AGTGTGTGCACGAGGCTGGGGAGTCTCGGACACCTGCATGTCGACCCAGCCA 166509
QY	222	GGGCTGTGTTGTCAGCCTGGGGCAGGCC 251
Db	166510	GGGCTGTGTTGTCAGCCTGGGGCAGGCC 166539

RESULT 10
AF126063

LOCUS	AF126063	1739 bp	mRNA	linear	ROD 12-OCT-1999
DEFINITION	Mus musculus connective tissue growth factor-like protein precursor (Ctgfl) mRNA, complete cds.				
ACCESSION	AF126063				
VERSION	AF126063.1	GI:4337059			
KEYWORDS	.				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1739) Kumar,S., Hand,A.T., Connor,J.R., Dodds,R.A., Ryan,P.J., Trill,J.J., Fisher,S.M., Nuttall,M.E., Lipschutz,D.B., Zou,C., Hwang,S.M., Volta,B.J., James,I.E., Rieman,D.J., Gowen,M. and Lee,J.C.				
TITLE	Identification and cloning of a connective tissue growth factor-like cDNA from human osteoblasts encoding a novel regulator of osteoblast functions				
JOURNAL	J. Biol. Chem. 274 (24), 17123-17131 (1999)				
MEDLINE	99287915				
PUBMED	10358067				
REFERENCE	2 (bases 1 to 1739) Kumar,S. and Zou,C.				
AUTHORS	Direct Submission				
TITLE	Submitted (04-FEB-1999) Bone & Cartilage Biology, UW 2109, Smithkline Beecham, 709 Swedeland Rd., King of Prussia, PA 19406, USA				
JOURNAL					

FEATURES

source

gene	Location/Qualifiers
CDS	1..1739 /organism="Mus musculus" /db_xref="taxon:10090" /tissue_type="lung" 1..1739 /gene="Ctgfl" 242..997 /gene="Ctgfl" /note="similar to the Mus musculus WISP-2 protein encoded by the sequence presented in GenBank Accession Number AF100778; putative growth factor; CTGF-L; contains IGF binding (IGFBP), Von Willebrand Factor type C (VWC) repeat and thrombospondin type I (TSP1) domains; member of the CCN (CTGF/Cyrl/Nov) family; lacks the fourth carboxy-terminal (CT) domain present in other members of the CCN family" /codon_start=1 /product="connective tissue growth factor-like protein precursor" /protein_id="AAD18058.1" /db_xref="GI:4337060" /translation="MRGNPLIHLELAISFLCILSMVYSOLCPAPCACPMTPPOCPGVP LVLDGCGCCRVCAARLIGESCDHLHVCDPSSQGLVCQPGAGPSGRGAVCLFEEDGSCVEY NGRRYLDGETFEKPNCRVLCRCDDGFTCLPLCSEDPVLPMDCPRPRIQVGRCPPE WVCDQAVMOPAIQPSAOGHQLSALVTPASADGPCPNWSTWGPCSTTCGLGIATRVSN NMRFCQLEIQRLCLSRPCLASRSHGSWNSAF"

BASE COUNT 375 a 480 c 489 g 395 t		
ORIGIN		
Query Match 10.6%; Score 80; DB 10; Length 1739;		
Best Local Similarity 100.0%; Pred. No. 5.2e-32;		
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	172	CGGAGGCTGGGGAGTCTCGGACACCTGCATGTCGACCCAGGCGCTGTT 231
Db	413	CGGAGGCTGGGGAGTCTCGGACACCTGCATGTCGACCCAGGCGCTGTT 472
QY	232	TGTCAGCCTGGGGCAGGCC 251
Db	473	TGTCAGCCTGGGGCAGGCC 492

RESULT 11
AR210337
LOCUS AR210337 738 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 38 from patent US 6387657.
ACCESSION AR210337
VERSION AR210337.1 GI:21512542
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 738)
Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 38 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..738
BASE COUNT 104 a 272 c 238 g 124 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 158
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Db 115 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 146

RESULT 12
LOCUS AR210338 841 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 39 from patent US 6387657.
ACCESSION AR210338
VERSION AR210338.1 GI:21512543
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 841)
Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J.,
Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 39 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..841
BASE COUNT 124 a 297 c 280 g 140 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGGATGCGCGCTGCCAGCTGGAGCTGCC 437
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Db 417 GAGGATGCGCGCTGCCAGCTGGAGCTGCC 448

RESULT 13
LOCUS AX076919 1266 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 31 from Patent WO0105836.
ACCESSION AX076919
VERSION AX076919.1 GI:13121575
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 0105836-A 31 25-JAN-2001;

FEATURES Genentech, Inc. (US)
source 1..1266
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 216 a 418 c 390 g 242 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 158
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Db 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

RESULT 14
LOCUS AX464186 1266 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 319 from Patent WO0140466.
ACCESSION AX464186
VERSION AX464186.1 GI:21899109
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source 1..1266
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 216 a 418 c 390 g 242 t
ORIGIN

Query Match 4.2%; Score 32; DB 6; Length 1266;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 158
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Db 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

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LOCUS AF083500 1283 bp mRNA linear PRI 04-NOV-1998
DEFINITION Homo sapiens connective tissue growth factor-like protein
precursor, mRNA, complete cds.
ACCESSION AF083500
VERSION AF083500.1 GI:3462835
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE

AUTHORS Kumar, S.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1998) Bone & Cartilage Biology, UW 2109,
SmithKline Beecham, 709 Swedeland Road, King of Prussia, PA 19406,
USA

FEATURES
source Location/Qualifiers
1.1283
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/db_xref="taxon:9606"
/chromosome="20"
/map="20q12-q13"
/cell_type="primary osteoblast"
9.761

CDS

/note="CTGF-L; encodes IGF binding (IGFB), Von Willebrand
factor type C (VWC) and thrombospondin type I (TSP1)
domains; member of the CCN (CTGF/cyrr61/nov) family; lacks
the fourth carboxy-terminal domain present in other
members of the CCN family"
/codon_start=1
/product="connective tissue growth factor-like protein
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/protein_id="AAC70350.1"
/db_xref="GI:3462836"
/translation="MRGTPKTHLAFSLCLLSKVRTQLCPPTCTCPWPPRCPLGVP
LVLDGCGCCRVCARLGEPCDOLHYCDASOGLVCOGAGPGRGALCLLAEDSSCEV
NGRLYREGETFQPHCSIRCRCEDEGFTCVPLCSEDEVRLPSWDCPHPRRVEVLGKCCE
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BASE COUNT 235 a 418 c 389 g 241 t
ORIGIN

Query Match 4.2%; Score 32; DB 9; Length 1283;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTCTGGATGGCTGTGGCTGCTG 158
|||||
Db 135 GTACCCCTGGTCTGGATGGCTGTGGCTGCTG 166

Search completed: July 28, 2003, 21:14:49
Job time : 2093.59 secs

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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:31:11 ; Search time 197.767 Seconds
(without alignments)
8574.520 Million cell updates/sec

Title: US-10-010-408-3
Perfect score: 753
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 segs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	100.0	753	20	AAZ07517
2	753	100.0	1708	20	AAZ07516
3	681	90.4	681	20	AAZ07521
4	210	27.9	210	20	AAZ07519
5	177	23.5	177	20	AAZ07518
6	174	23.1	174	20	AAZ07520
7	90	12.0	753	20	AAZ76489
8	90	12.0	1734	20	AAZ76488
9	32	4.2	199	22	ABA72245

10	32	4.2	199	22	ABA38112	Probe #16578 for g
11	32	4.2	199	22	AAK20667	Human brain expres
12	32	4.2	199	22	AAK46811	Human bone marrow
13	32	4.2	199	22	AAI25749	Probe #15682 for g
14	32	4.2	199	22	AAI52650	Probe #21336 used
15	32	4.2	199	24	ABS21124	Human genome-deriv
16	32	4.2	586	22	ABA59703	Human foetal liver
17	32	4.2	586	22	ABA28232	Probe #6698 for ge
18	32	4.2	586	22	AAK07972	Human brain expres
19	32	4.2	586	22	AAK33842	Human bone marrow
20	32	4.2	586	22	AAI16552	Probe #6485 for ge
21	32	4.2	586	22	AAI39568	Probe #8254 used t
22	32	4.2	586	24	ABS08689	Human genome-deriv
23	32	4.2	738	20	AAZ76501	Human WISP-2 prote
24	32	4.2	750	20	AAZ76487	Human WISP-2 prote
25	32	4.2	841	20	AAZ76502	Human WISP-2 prote
26	32	4.2	1257	20	AAZ28435	EGF-like homologue
27	32	4.2	1266	21	AAA30048	Human PRO261 nucle
28	32	4.2	1266	22	AAZ21403	Human cDNA sequenc
29	32	4.2	1266	22	AAZ60368	PRO261 coding sequ
30	32	4.2	1266	22	AAZ97451	Human angiogenesis
31	32	4.2	1267	21	AAZ77566	Human PRO261 cDNA
32	32	4.2	1285	19	AAZ29260	Human connective t
33	32	4.2	1293	20	AAZ76486	Human WISP-2 prote
34	32	4.2	1309	22	AAH28214	Connective tissue
35	32	4.2	1337	22	AAH46952	Human secreted pro
36	32	4.2	1352	22	AAH46936	Human secreted pro
37	32	4.2	1522	20	AAZ16595	Human growth facto
38	32	4.2	2136	22	AAK94706	Human full-length
39	32	4.2	13255	22	AAK76842	Human immune/haema
40	27	3.6	51	20	AAZ76535	Human WISP-2 probe
41	27	3.6	51	21	AAZ7569	Human PRO261 hybr1
42	27	3.6	51	21	AAA30051	Probe for PRO261 n
43	27	3.6	51	22	AAZ60371	PRO261 probe #1.
44	27	3.6	51	22	AAZ97454	Human PRO261 hybr1
45	23	3.1	634	22	AAK91750	Human cDNA 5'-end

ALIGNMENTS

RESULT 1	
AAZ07517	AAZ07517 standard; cDNA; 753 BP.
XX	
AC	AAZ07517;
XX	
DT	26-NOV-1999 (first entry)
XX	
DE	Rat HICP polypeptide coding sequence.
XX	
KW	Heparin-induced CGN-like protein; HICP; cell-associated activity; ss;
KW	cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
XX	
OS	Rattus sp.
XX	
PN	W09947556-A2.
XX	
PD	23-SEP-1999.
XX	
PF	18-MAR-1999; 99WO-US05999.
XX	
PR	19-MAR-1998; 98US-0044273.
XX	
PA	(TUFT) TUFTS COLLEGE.
XX	
PI	Castellot UJ;
XX	
DR	WPI; 1999-562060/47.
DR	P-PSDB; AAY27434.
XX	
PT	Nucleic acid sequences encoding rat heparin-induced CGN-like protein, used in methods to identify modulators or in diagnostic applications

XX Claim 5; Fig 1; 108pp; English.
XX
CC The invention provides a rat heparin-induced CN-like protein (HICP)
CC protein. Agents that stimulate or inhibit HICP protein activity or
CC expression, antisense HICP nucleic acid molecules, and HICP antibodies,
CC can be used to modulate cell-associated activity. HICP modulators can be
CC used to treat disorders characterized by aberrant HICP protein activity
CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
CC specific for HICP can be used to detect HICP activity in a biological
CC sample. HICP can be used to treat disorders, such as a cardiovascular or
CC fibrotic disorder, characterized by aberrant cell proliferation. The
CC present sequence represents the coding sequence of rat HICP.
XX
SQ Sequence 753 BP; 132 A; 235 C; 230 G; 156 T; 0 other;

Query Match 100.0%; Score 753; DB 20; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGGACGCCCACTGATCCATCTTCGGCCACTTCCCTTCGCTCTCTCATG 60
DB 1 ATGAGGGGACGCCCACTGATCCATCTTCGGCCACTTCCCTTCGCTCTCTCATG 60
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DB 61 GTGTGTGCCCACTGTGCCGACACCCCTGTACCTGTCTTGACACACCCCAAGTCCCA 120
QY 121 CAGGGGTTACCCCTGTGTGCTGGATGGCTGTGCTGTAAAGTGTGTGACAGGAGCTG 180
DB 121 CAGGGGTTACCCCTGTGTGCTGGATGGCTGTGCTGTAAAGTGTGTGACAGGAGCTG 180
QY 121 CAGGGGTTACCCCTGTGTGCTGGATGGCTGTGCTGTAAAGTGTGTGACAGGAGCTG 180
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DB 181 GGGAGTCTGCGACACCACTGCAATGTGCGACCCAGCGAGGCGCTTGTTCAGCCT 240
QY 181 GGGAGTCTGCGACACCACTGCAATGTGCGACCCAGCGAGGCGCTTGTTCAGCCT 240
DB 181 GGGAGTCTGCGACACCACTGCAATGTGCGACCCAGCGAGGCGCTTGTTCAGCCT 240
QY 241 GGGGACAGCCCTGGCGCCATGGGGCTGTGTCTCTTGATGAGATGACGGTAGCTGT 300
DB 241 GGGGACAGCCCTGGCGCCATGGGGCTGTGTCTCTTGATGAGATGACGGTAGCTGT 300
QY 301 GAGGTGAATGGCCCGCAGGTACCTGATGGAGAGACCTTTAAACCAATTGCAGGGTCTG 360
DB 301 GAGGTGAATGGCCCGCAGGTACCTGATGGAGAGACCTTTAAACCAATTGCAGGGTCTG 360
QY 361 TGCCGCTGTGATGACGGGTTCACCTGCTGCGGCTGTGACAGTATGCGGCTG 420
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DB 601 TGGGGCCCTGCTCAACCACTGTGGCTGGGCATAGCGAACCCGAGTGTCCAACAGAAC 660
QY 661 CGATTCTGCGCAACTGGAGATCCAAAGCGGCTGTGTGCGCCACAGACCTGCTGGCAGCC 720
DB 661 CGATTCTGCGCAACTGGAGATCCAAAGCGGCTGTGTGCGCCACAGACCTGCTGGCAGCC 720
QY 721 AGAGGCACAGCTCATGGAACAGTGTCTTCTAA 753
DB 721 AGAGGCACAGCTCATGGAACAGTGTCTTCTAA 753

RESULT 2
AAZ07516
ID AAZ07516 standard; cDNA; 1708 BP.
XX
AC AAZ07516;
XX
DT 26-NOV-1999 (first entry)
XX
DE Rat HICP polypeptide encoding cDNA.
XX
KM Heparin-induced CN-like protein; HICP; cell-associated activity; ss;
XX cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
OS Rattus sp.
XX
PN WO9947556-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-US05999.
XX
PR 19-MAR-1998; 98US-0044273.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Castellot JJ;
XX
DR WPI; 1999-562060/47.
DR P-PSDB; AAY27434.
XX
PT Nucleic acid sequences encoding rat heparin-induced CN-like protein,
PT used in methods to identify modulators or in diagnostic applications
XX
PS Claim 2; Fig 1; 108pp; English.
XX
CC This cDNA encodes a rat heparin-induced CN-like protein (HICP) protein.
CC Agents that stimulate or inhibit HICP protein activity or expression,
CC antisense HICP nucleic acid molecules and HICP antibodies, can be used to
CC modulate cell-associated activity. HICP modulators can be used to treat
CC disorders characterized by aberrant HICP protein activity or expression.
CC Probes capable of hybridizing to HICP mRNA or antibodies specific for
CC HICP can be used to detect HICP activity in a biological sample. HICP
CC can be used to treat disorders, such as a cardiovascular or fibrotic
CC disorder, characterized by aberrant cell proliferation.
XX
SQ Sequence 1708 BP; 362 A; 486 C; 478 G; 382 T; 0 other;

Query Match 100.0%; Score 753; DB 20; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGGACGCCCACTGATCCATCTTCGGCCACTTCCCTTCGCTCTCTCATG 60
DB 249 ATGAGGGGACGCCCACTGATCCATCTTCGGCCACTTCCCTTCGCTCTCTCATG 308
QY 61 GTGTGTGCCCACTGTGCCGACACCCCTGTACCTGTCTTGACACACCCAGTGCCCA 120
DB 309 GTGTGTGCCCACTGTGCCGACACCCCTGTACCTGTCTTGACACACCCAGTGCCCA 368
QY 121 CAGGGGTTACCCCTGTGTGCTGGATGGCTGTGCTGTAAAGTGTGTGACAGGAGCTG 180
DB 369 CAGGGGTTACCCCTGTGTGCTGGATGGCTGTGCTGTAAAGTGTGTGACAGGAGCTG 428
QY 181 GGGAGTCTGCGACACCACTGCAATGTGCGACCCAGCGAGGCGCTTGTTCAGCCT 240
DB 429 GGGAGTCTGCGACACCACTGCAATGTGCGACCCAGCGAGGCGCTTGTTCAGCCT 488
QY 241 GGGGACAGCCCTGGCGCCATGGGGCTGTGTCTCTTGATGAGATGACGGTAGCTGT 300
DB 489 GGGGACAGCCCTGGCGCCATGGGGCTGTGTCTCTTGATGAGATGACGGTAGCTGT 548
QY 301 GAGGTGAATGGCCCGCAGGTACCTGATGGAGAGACCTTTAAACCAATTGCAGGGTCTG 360
DB 301 GAGGTGAATGGCCCGCAGGTACCTGATGGAGAGACCTTTAAACCAATTGCAGGGTCTG 360

Db 549 GAGGTGAATGCCCCGAGGTACCTGGATGGAAGAGACCTTTAAACCAATTGCAGGGTCTG 608
QY 361 TGCCCGCTGTATGACGGGTGGCTTCACTGCTGCCGCTGTGAGTGAGGATGTGGGGCTG 420
Db 609 TGCCCGCTGTATGACGGGTGGCTTCACTGCTGCCGCTGTGAGTGAGGATGTGGGGCTG 668
QY 421 CCCAGCTGGGACTGCCACGCGCCCAAGAGAATACAGGTGCGCAGAAAGTGCTGCCCGAG 480
Db 669 CCCAGCTGGGACTGCCACGCGCCCAAGAGAATACAGGTGCGCAGAAAGTGCTGCCCGAG 728
QY 481 TGGGTATGTGACCAGGAGGTGACACCGGGCATCCAGCGCTCCACGGCGCAAGACACCAA 540
Db 729 TGGGTATGTGACCAGGAGGTGACACCGGGCATCCAGCGCTCCACGGCGCAAGACACCAA 788
QY 541 CTTTCTGCCCCCTGTCTACTCCTGCTCTGTGATGCTCCTTGTCCAAATTGGAGCACAGCC 600
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QY 601 TGGGGCCCCCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCGAGTGTCCAACCAGAAC 660
Db 849 TGGGGCCCCCTGCTCAACCACCTGTGGGCTGGGCATAGCCACCGAGTGTCCAACCAGAAC 908
QY 661 CGATTCTGCCAACTGGAGATCCAACGCGCTGTGTGTGCCCAGACCCTGCTGGCAGCC 720
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QY 721 AGGAGCCACAGCTCATGGAACAGTGTCTTCTAA 753
Db 969 AGGAGCCACAGCTCATGGAACAGTGTCTTCTAA 1001

RESULT 3
AAZ07521
ID AAZ07521 standard; cDNA; 681 BP.
XX
AC AAZ07521;
XX
DT 26-NOV-1999 (first entry)
XX
DE Rat HICP mature polypeptide coding sequence.
XX
KW Heparin-induced CN-like protein; HICP; cell-associated activity; ss;
KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder.
XX
OS Rattus sp.
XX
PN WO9947556-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-US05999.
XX
PR 19-MAR-1998; 98US-0044273.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Castellot JJ;
XX
DR WPI; 1999-562060/47.
DR P-PSDB; AAY27440.
XX

Nucleic acid sequences encoding rat heparin-induced CN-like protein,
used in methods to identify modulators or in diagnostic applications -
Disclosure; Fig 2; 108pp; English.

CC The invention provides a rat heparin-induced CN-like protein (HICP)
CC protein. Agents that stimulate or inhibit HICP protein activity or
CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
CC can be used to modulate cell-associated activity. HICP modulators can be
CC used to treat disorders characterized by aberrant HICP protein activity
CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
CC specific for HICP can be used to detect HICP activity in a biological

CC sample. HICP can be used to treat disorders, such as a cardiovascular or
CC fibrotic disorder, characterized by aberrant cell proliferation. The
CC present sequence represents the coding sequence of rat HICP mature
CC polypeptide.

SQ Sequence 681 BP; 121 A; 211 C; 215 G; 134 T; 0 other;

Query Match 90.4%; Score 681; DB 20; Length 681;
Best Local Similarity 100.0%; Pred. No. 2.4e-312;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAGCTGTGCCGGACACACCTGTACTGTCTTGACACACACCCAGTGCCACAGGGGTA 60
QY 130 CCCCTGTGCTGTGATGGCTGTGGCTGCTGTAAGTGTGTGCACGGAGGCTGGGGAGTCC 189
Db 61 CCCCTGTGCTGTGATGGCTGTGGCTGCTGTAAGTGTGTGCACGGAGGCTGGGGAGTCC 120
QY 190 TGGCAGCACCTGCATGTCTGCGACCCACGACAGGCGCTGGTTGTACAGCTGGGGCAGGC 249
Db 121 TGGCAGCACCTGCATGTCTGCGACCCACGACAGGCGCTGGTTGTACAGCTGGGGCAGGC 180
QY 250 CCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGGATGACGCTGTGAGGTGAAT 309
Db 181 CCTGGCGGCATGGGGCTGTGTCTCTTGGATGAGGATGACGCTGTGAGGTGAAT 240
QY 310 GGCCGACAGTACCTGGATGAGAGACCTTTAAACCAATTCAGGCTCTGTGCCGCTGT 369
Db 241 GGCCGACAGTACCTGGATGAGAGACCTTTAAACCAATTCAGGCTCTGTGCCGCTGT 300
QY 370 GATGAGGTGGCTTACCTGCCCTGCGCTGTGCAGTGAAGATGTGCGGCTGCCAGCTGG 429
Db 301 GATGAGGTGGCTTACCTGCCCTGCGCTGTGCAGTGAAGATGTGCGGCTGCCAGCTGG 360
QY 430 GACTGCCACAGCCCCAAGAGATACAGGTGCCAGGAAGTCTGCCCGAGTGGTATGT 489
Db 361 GACTGCCACAGCCCCAAGAGATACAGGTGCCAGGAAGTCTGCCCGAGTGGTATGT 420
QY 490 GACCAGGAGTGACACCGCGCATCCAGCGCTCCACGGCGCAAGGACACCACTTCTGCC 549
Db 421 GACCAGGAGTGACACCGCGCATCCAGCGCTCCACGGCGCAAGGACACCACTTCTGCC 480
QY 550 CTTGTCACTCCTGCCCTGTGTGATGCTCCTGTGCCAAATTGAGACACAGCCTGGGCCCC 609
Db 481 CTTGTCACTCCTGCCCTGTGTGATGCTCCTGTGCCAAATTGAGACACAGCCTGGGCCCC 540
QY 610 TGTCAACACACCTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACAGACCATTTCTGC 669
Db 541 TGTCAACACACCTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACAGACCATTTCTGC 600
QY 670 CAACTGGAGATCCACAGCGCGCTGTGTCTGCCAGACCTGCTGGCAGCCAGAGCCAC 729
Db 601 CAACTGGAGATCCACAGCGCGCTGTGTCTGCCAGACCTGCTGGCAGCCAGAGCCAC 660
QY 730 AGCTCATGGAACAGTGTTC 750
Db 661 AGCTCATGGAACAGTGTTC 681

RESULT 4
AAZ07519
ID AAZ07519 standard; cDNA; 210 BP.
XX
AC AAZ07519;
XX
DT 26-NOV-1999 (first entry)
XX
DE Rat HICP IGFBP domain encoding cDNA.

KW Heparin-induced CN-like protein; HICP; cell-associated activity; ss;
KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;
KW insulin-like growth factor binding protein; IGFBP.

```
XX OS Rattus sp.
XX PN WO9947556-A2.
XX PD 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-US05999.
XX PR 19-MAR-1998; 98US-0044273.
XX PA (TUFT ) TUFTS COLLEGE.
XX PI Castellot JI;
XX DR WPI; 1999-562060/47.
XX DR P-PSDB; AAY27438.
XX PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
XX PS used in methods to identify modulators or in diagnostic applications
XX PS Disclosure; Page 104; 108pp; English.
XX CC The invention provides a rat heparin-induced CCN-like protein (HICP)
XX CC protein. Agents that stimulate or inhibit HICP protein activity or
XX CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
XX CC can be used to modulate cell-associated activity. HICP modulators can be
XX CC used to treat disorders characterized by aberrant HICP protein activity
XX CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
XX CC specific for HICP can be used to detect HICP activity in a biological
XX CC sample. HICP can be used to treat disorders, such as a cardiovascular or
XX CC fibrotic disorder, characterized by aberrant cell proliferation. The
XX CC present sequence represents a nucleotide sequence encoding the insulin-
XX CC like growth factor binding protein (IGFBP) domain of HICP polypeptide.
SQ Sequence 210 BP; 27 A; 65 C; 74 G; 44 T; 0 other;
Query Match 27.9%; Score 210; DB 20; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 70 CAGCTGTGCCGACACCCCTGTAACCTGCTTGGACACACCCAGTGCCACAGGGGTA 129
DB 1 CAGCTGTGCCGACACCCCTGTAACCTGCTTGGACACACCCAGTGCCACAGGGGTA 60
OY 130 CCCCTGTGCTGATGGCTGTGCTGCTGTAAGTGTGTGACGAGGCTGGGGAGTCC 189
DB 61 CCCCTGTGCTGATGGCTGTGCTGCTGTAAGTGTGTGACGAGGCTGGGGAGTCC 120
OY 190 TGGGACACACCTGATGTGTGACCCACGACGAGGCTGTTTGTCAAGCTGGGGCAGGC 249
DB 121 TGGGACACACCTGATGTGTGACCCACGACGAGGCTGTTTGTCAAGCTGGGGCAGGC 180
OY 250 CCTGGCGGCGCATGGGGCTGTGCTCTTG 279
DB 181 CCTGGCGGCGCATGGGGCTGTGCTCTTG 210
RESULT 5
AAZ07518
ID AAZ07518 standard; cDNA; 177 BP.
XX AC AAZ07518;
XX DT 26-NOV-1999 (first entry)
XX DE Rat HICP VWC domain encoding cDNA.
XX KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;
XX KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;
XX KW Von Willebrand C domain; VWC.
OS Rattus sp.
```

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XX PN WO9947556-A2.
XX PD 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-US05999.
XX PR 19-MAR-1998; 98US-0044273.
XX PA (TUFT ) TUFTS COLLEGE.
XX PI Castellot JI;
XX DR WPI; 1999-562060/47.
XX DR P-PSDB; AAY27436.
XX PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
XX PS used in methods to identify modulators or in diagnostic applications
XX PS Disclosure; Page 103; 108pp; English.
XX CC The invention provides a rat heparin-induced CCN-like protein (HICP)
XX CC protein. Agents that stimulate or inhibit HICP protein activity or
XX CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
XX CC can be used to modulate cell-associated activity. HICP modulators can be
XX CC used to treat disorders characterized by aberrant HICP protein activity
XX CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
XX CC specific for HICP can be used to detect HICP activity in a biological
XX CC sample. HICP can be used to treat disorders, such as a cardiovascular or
XX CC fibrotic disorder, characterized by aberrant cell proliferation. The
XX CC present sequence represents a cDNA encoding the Von Willebrand C (VWC)
XX CC a domain of the HICP polypeptide.
SQ Sequence 177 BP; 35 A; 47 C; 60 G; 35 T; 0 other;
Query Match 23.5%; Score 177; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.8e-74;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 298 TGTGAGGTGAATGCCGACGTAACCTGATGAGAGACCTTAAACCAATTGCAGGTC 357
DB 1 TGTGAGGTGAATGCCGACGTAACCTGATGAGAGACCTTAAACCAATTGCAGGTC 60
OY 358 CTGTGCGCTGTGATGACGGTGGCTTACCTGCCCTGCCGTGTGACAGTGAAGTGGCG 417
DB 61 CTGTGCGCTGTGATGACGGTGGCTTACCTGCCCTGCCGTGTGACAGTGAAGTGGCG 120
OY 418 CTGCCAGCTGGGACTGCCACGCCCCAAGAGATACAGTGCAGGAAGTCTGC 474
DB 121 CTGCCAGCTGGGACTGCCACGCCCCAAGAGATACAGTGCAGGAAGTCTGC 177
RESULT 6
AAZ07520
ID AAZ07520 standard; cDNA; 174 BP.
XX AC AAZ07520;
XX DT 26-NOV-1999 (first entry)
XX DE Rat HICP TSPI domain encoding cDNA.
XX KW Heparin-induced CCN-like protein; HICP; cell-associated activity; ss;
XX KW cardiovascular disorder; aberrant cell proliferation; fibrotic disorder;
XX KW thrombospondin 1 domain; TSPI.
OS Rattus sp.
XX PN WO9947556-A2.
XX PD 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-US05999.
```

XX 19-MAR-1998; 98US-0044273.
PR (TUFT) TUFTS COLLEGE.
XX
XX Castellot JJ;
PI
XX
XX WPI; 1999-562060/47.
DR P-PSDB; AAX27439.
XX
PT Nucleic acid sequences encoding rat heparin-induced CCN-like protein,
PT used in methods to identify modulators or in diagnostic applications
XX
PS Disclosure; Page 105; 108pp; English.
XX
XX The invention provides a rat heparin-induced CCN-like protein (HICP)
CC protein. Agents that stimulate or inhibit HICP protein activity or
CC expression, antisense HICP nucleic acid molecules and HICP antibodies,
CC can be used to modulate cell-associated activity. HICP modulators can be
CC used to treat disorders characterized by aberrant HICP protein activity
CC or expression. Probes capable of hybridizing to HICP mRNA or antibodies
CC specific for HICP can be used to detect HICP activity in a biological
CC sample. HICP can be used to treat disorders, such as a cardiovascular or
CC fibrotic disorder, characterized by aberrant cell proliferation. The
CC present sequence represents a nucleotide sequence encoding the
CC thrombospondin 1 (TSP1) domain of the HICP polypeptide.
XX
SQ Sequence 174 BP; 36 A; 62 C; 45 G; 31 T; 0 other;

Query Match 23.1%; Score 174; DB 20; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-72;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 577 CCTGTGCCAATTGAGACACAGCTGGGGCCCTGCTCAACCACTGTGGCTGGGCATA 636
Db 1 CCTGTGCCAATTGAGACACAGCTGGGGCCCTGCTCAACCACTGTGGCTGGGCATA 60

QY 637 GCCACCCGAGTGTCCAACCAAGCATTTCTGCCAACTGAGATCCAAAGCCGCTGTGT 696
Db 61 GCCACCCGAGTGTCCAACCAAGCATTTCTGCCAACTGAGATCCAAAGCCGCTGTGT 120

QY 697 CTGCCAGACCCCTGCTGGCAGCCAGAGCCACAGCTCATGACAGTGTCTTC 750
Db 121 CTGCCAGACCCCTGCTGGCAGCCAGAGCCACAGCTCATGACAGTGTCTTC 174

RESULT 7
AAX76489/c
ID AAX76489 standard; DNA; 753 BP.
XX
AC AAX76489;
XX
DT 06-AUG-1999 (first entry)
XX
DE Mouse WISP-2 protein complementary nucleotide sequence SEQ ID NO:18.
XX
KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;
KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
KW connective tissue disorder; catabolic state; inflammation;
KW testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
OS Mus sp.
XX
PN WO9921998-A1.
XX
PD 06-MAY-1999.
XX
PF 29-OCT-1998; 98WO-US22991.
XX
PR 14-APR-1998; 98US-0081695.

PR 29-OCT-1997; 97US-0063704.
PR 03-FEB-1998; 98US-0073612.
XX
XX (GETH) GENENTECH INC.
PA
XX Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX
XX WPI; 1999-337420/28.
DR
XX
PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
PT
XX
XX Disclosure; Page 179-180; 284pp; English.
PS
XX
XX The present invention describes Wnt-1 induced secreted polypeptides,
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
CC and WISP-3 have homology to connective tissue growth factor (CTGF).
CC Products from the present invention can be used to treat WISP-related
CC disorders such as breast, ovarian, and colon cancer or melanoma. The
CC products can be used to treat arteriosclerosis. The products can also be
CC used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and
CC blastocoele disorders, haematopoiesis-related disorders, tissue-growth
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
CC cells.
XX
SQ Sequence 753 BP; 159 A; 229 C; 238 G; 127 T; 0 other;

Query Match 12.0%; Score 90; DB 20; Length 753;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGACACGAGAGCTGGGGAGTCTCGACACCACTGCATGTCTGCAGCCAGCCA 221
Db 592 AGTGTGACACGAGAGCTGGGGAGTCTCGACACCACTGCATGTCTGCAGCCAGCCA 533

QY 222 GGGCCTGTGTTGTCAAGCTGGGGCGAGGCC 251
Db 532 GGGCCTGTGTTGTCAAGCTGGGGCGAGGCC 503

RESULT 8
AAX76488
ID AAX76488 standard; DNA; 1734 BP.
XX
AC AAX76488;
XX
DT 06-AUG-1999 (first entry)
XX
DE Mouse WISP-2 protein nucleotide sequence SEQ ID NO:17.
XX
KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;
KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
KW connective tissue disorder; catabolic state; inflammation;
KW testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
OS Mus sp.
XX
PN WO9921998-A1.
XX
PD 06-MAY-1999.


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XX 29-OCT-1998; 98WO-US22991.
PF 14-APR-1998; 98US-0081695.
XX 29-OCT-1997; 97US-0063704.
PR 03-FEB-1998; 98US-0073612.
XX (GETH ) GENENTECH INC.
XX Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX WPI; 1999-337420/28.
DR P-PSDB; AAY17651.
XX
XX New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
PT Example 2; Page 178-179; 284pp; English.
XX
XX The present invention describes Wnt-1 induced secreted polypeptides,
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
CC and WISP-3 have homology to connective tissue growth factor (CTGF).
CC Products from the present invention can be used to treat WISP-related
CC disorders such as breast, ovarian, and colon cancer or melanoma. The
CC products can be used to treat arteriosclerosis. The products can also be
CC used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal, and
CC blastocoealic disorders, haematopoesis-related disorders, tissue-growth
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
CC cells.
XX
XX Sequence 1734 BP; 355 A; 491 C; 495 G; 393 T; 0 other;
SQ
Query Match 12.0%; Score 90; DB 20; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 162 AGTGTGTGCACGAGGCTGGGGAGTCTCTGCGACCACCTGCACTCTGCGAGCCAGCCCA 221
DB 418 AGTGTGTGCACGAGGCTGGGGAGTCTCTGCGACCACCTGCACTCTGCGAGCCAGCCCA 477
OY 222 GGGCCTGCTTGTCTCAGCCTGGGCGAGGCC 251
DB 478 GGGCCTGCTTGTCTCAGCCTGGGCGAGGCC 507
RESULT 9
ABA72245
ID ABA72245 standard; DNA; 199 BP.
XX
AC ABA72245;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #20550.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
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PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 4; SEQ ID NO 20550; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
SQ
Query Match 4.2%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 406 GAGATGTGCGGCTGCCAGCTGGGACTGCC 437
DB 129 GAGATGTGCGGCTGCCAGCTGGGACTGCC 160
RESULT 10
ABA38112
ID ABA38112 standard; DNA; 199 BP.
XX
AC ABA38112;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #16578 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
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XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
DR WPI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX PS Claim 4; SEQ ID NO 16578; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match
Best Local Similarity 4.2%; Score 32; DB 22; Length 199;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 406 GAGGATGCGGGCTGCCAGCTGGGACTGCC 437
Db 129 GAGGATGCGGGCTGCCAGCTGGGACTGCC 160

RESULT 11
AAK20667
ID AAK20667 standard; DNA; 199 BP.
XX AC AAK20667;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 20658.
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00667.
XX PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483446/52.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
```

```
PS Example 4; SEQ ID NO: 20658; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match
Best Local Similarity 4.2%; Score 32; DB 22; Length 199;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 406 GAGGATGCGGGCTGCCAGCTGGGACTGCC 437
Db 129 GAGGATGCGGGCTGCCAGCTGGGACTGCC 160

RESULT 12
AAK46811
ID AAK46811 standard; DNA; 199 BP.
XX AC AAK46811;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 21368.
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00668.
XX PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX PS Example 4; SEQ ID NO: 21368; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;

Query Match
Best Local Similarity 4.2%; Score 32; DB 22; Length 199;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 406 GAGGATGCGGCTGCCAGCTGGGACTGCC 437
DB 129 GAGGATGCGGCTGCCAGCTGGGACTGCC 160
RESULT 13
AAI25749
ID AAI25749 standard; DNA; 199 BP.
AC AAI25749;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #15682 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PI 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 15682; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
Query Match 4.2%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 17-OCT-2001 (first entry)
XX
DE Probe #21336 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PI 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-48897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 21336; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 199 BP; 32 A; 65 C; 73 G; 29 T; 0 other;
Query Match 4.2%; Score 32; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 406 GAGGATGCGGCTGCCAGCTGGGACTGCC 437
DB 129 GAGGATGCGGCTGCCAGCTGGGACTGCC 160
RESULT 15
ABS21124
ID ABS21124 standard; DNA; 199 BP.
XX
AC ABS21124;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 21115.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 14:50:06 ; Search time 41.1485 Seconds
(without alignments)
5612.050 Million cell updates/sec

Title: US-10-010-408-3
Perfect score: 753
Sequence: 1 ATGAGGGGACGCCACTGAT.....CATGACAGTCTTCTTAA 753

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	12.0	1734	4	US-09-182-145-17
2	90	12.0	1734	4	US-09-182-145-18
3	32	4.2	738	4	US-09-182-145-38
4	32	4.2	841	4	US-09-182-145-39
5	32	4.2	1293	4	US-09-182-145-13
6	32	4.2	1293	4	US-09-182-145-14
7	27	3.6	51	4	US-09-182-145-117
8	19	2.5	616	4	US-09-385-982-220
9	19	2.5	1196	4	US-09-149-476-225
10	19	2.5	1220	4	US-09-149-476-57
11	19	2.5	1514	2	US-09-213-768-1
12	19	2.5	1539	4	US-09-668-680-13
13	18	2.4	20	2	US-09-213-768-2
14	18	2.4	3727	1	US-08-249-380-1
15	17	2.3	44	4	US-09-182-145-152
16	17	2.3	464	2	US-08-691-814B-117
17	17	2.3	480	3	US-09-188-930-206
18	17	2.3	482	2	US-08-691-814B-120
19	17	2.3	614	4	US-08-998-416-151
20	17	2.3	896	3	US-09-188-930-36
21	17	2.3	933	3	US-08-987-743-1
22	17	2.3	1308	3	US-08-987-743-5
23	17	2.3	1743	3	US-08-665-259-20
24	17	2.3	1743	3	US-08-762-500-20
25	17	2.3	1821	4	US-09-149-476-90
26	17	2.3	1974	3	US-08-762-500-78
27	17	2.3	2329	1	US-08-455-559-9

C	28	17	2.3	2329	4	US-09-145-060-9	Sequence 9, Appl1
C	29	17	2.3	2329	5	PCR-US94-00657-9	Sequence 9, Appl1
	30	17	2.3	2517	3	US-08-733-360A-4	Sequence 4, Appl1
	31	17	2.3	2517	3	US-08-987-743-16	Sequence 16, Appl1
	32	17	2.3	2517	4	US-08-916-935-4	Sequence 4, Appl1
	33	17	2.3	3865	4	US-09-149-476-296	Sequence 296, App
C	34	17	2.3	6803	3	US-08-665-259-19	Sequence 19, Appl
C	35	17	2.3	6803	3	US-08-762-500-19	Sequence 19, Appl
	36	17	2.3	7874	4	US-09-780-175-96	Sequence 96, Appl
	37	17	2.3	81001	4	US-09-750-580-1	Sequence 1, Appl1
C	38	16	2.1	21	4	US-08-477-928A-27	Sequence 27, Appl
C	39	16	2.1	31	1	US-08-524-757-34	Sequence 34, Appl
	40	16	2.1	366	4	US-09-660-552-30	Sequence 30, Appl
	41	16	2.1	424	4	US-09-280-116-206	Sequence 206, App
	42	16	2.1	435	4	US-09-397-787-280	Sequence 280, App
C	43	16	2.1	441	4	US-09-660-552-28	Sequence 28, Appl
C	44	16	2.1	465	4	US-09-149-476-12	Sequence 12, Appl
C	45	16	2.1	524	4	US-09-149-476-199	Sequence 199, App

ALIGNMENTS

RESULT 1
US-09-182-145-17
Sequence 17, Application US/09182145B
Patent No. 6387657
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 17
LENGTH: 1734
TYPE: DNA
ORGANISM: Mus musculus
US-09-182-145-17

Query Match 12.0%; Score 90; DB 4; Length 1734;
Best local Similarity 100.0%; Pred. No. 6.8e-34;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTACACGAGGCTGGGGAGTCTGCGACCACTGATGTCTGCGACCCAGCCA 221
DB 418 AGTGTGTACACGAGGCTGGGGAGTCTGCGACCACTGATGTCTGCGACCCAGCCA 477

QY 222 GGCGCTGTGTGTGTCAGCCCTGGGGCAGGCC 251
DB 478 GGCGCTGTGTGTGTCAGCCCTGGGGCAGGCC 507

RESULT 2
US-09-182-145-18/C
Sequence 18, Application US/09182145B
Patent No. 6387657
GENERAL INFORMATION:

APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 18
LENGTH: 1734
TYPE: DNA
ORGANISM: Mus musculus
US-09-182-145-18

Query Match 12.0%; Score 90; DB 4; Length 1734;
Best Local Similarity 100.0%; Pred. No. 6.8e-34;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTCACGAGAGGCTGGGGAGTCTCGACACCTGCATGCTCGACCCAGCCCA 221
|||||
DB 1317 AGTGTGTCACGAGAGGCTGGGGAGTCTCGACACCTGCATGCTCGACCCAGCCCA 1258
|||||
QY 222 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 251
|||||
DB 1257 GGGCCTGTTTGTTCAGCCTGGGGCAGGCC 1228
|||||

RESULT 3

US-09-182-145-38
Sequence 38, Application US/09182145B
Patent No. 6387657
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 38
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapiens
US-09-182-145-38

Query Match 4.2%; Score 32; DB 4; Length 738;

Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 127 GTACCCCTGCTGTGATGGCTGTGCTG 158
|||||
DB 115 GTACCCCTGCTGTGATGGCTGTGCTG 146
|||||

RESULT 4

US-09-182-145-39
Sequence 39, Application US/09182145B
Patent No. 6387657
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 39
LENGTH: 841
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1-841
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6387657
US-09-182-145-39

Query Match 4.2%; Score 32; DB 4; Length 841;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGATGTGGGCTGCCAGCTGGGACTGCC 437
|||||
DB 417 GAGATGTGGGCTGCCAGCTGGGACTGCC 448
|||||

RESULT 5

US-09-182-145-13
Sequence 13, Application US/09182145B
Patent No. 6387657
GENERAL INFORMATION:
APPLICANT: Botstein, David A.
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29

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; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 13
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-13
```

```
Query Match          4.2%; Score 32; DB 4; Length 1293;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      127 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 158
Db      148 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 179
```

```
RESULT 6
US-09-182-145-14/c
; Sequence 14, Application US/09182145B
; Patent No. 6387657
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 14
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-182-145-14
```

```
Query Match          4.2%; Score 32; DB 4; Length 1293;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      127 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 158
Db      1146 GTACCCCTGTGCTGGATGGCTGTGGCTGCTG 1115
```

```
RESULT 7
US-09-182-145-117
; Sequence 117, Application US/09182145B
; Patent No. 6387657
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
```

```
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 117
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial sequence
```

```
; FEATURE:
```

```
; NAME/KEY: misc-feature
```

```
; LOCATION: 1-51
```

```
; OTHER INFORMATION: Sequence is synthesized.
```

```
; Patent No. 6387657
US-09-182-145-117
```

```
Query Match          3.6%; Score 27; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      132 CCTGTGCTGATGGCTGTGGCTGCTG 158
Db      1 CCTGTGCTGATGGCTGTGGCTGCTG 27
```

```
RESULT 8
US-09-385-982-220/c
```

```
; Sequence 220, Application US/09385982
```

```
; Patent No. 6262334
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(616)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-220
```

```
Query Match          2.5%; Score 19; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      369 TGATGACGGTGGCTTCACC 387
Db      127 TGATGACGGTGGCTTCACC 109
```

RESULT 9
US-09-149-476-225/c
; Sequence 225, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11

;; EARLIER APPLICATION NUMBER: 60/043,568
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,314
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,569
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,311
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,671
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,674
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,669
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,312
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,313
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,672
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,315
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/056,886
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,877
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,889
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;; EARLIER APPLICATION NUMBER: 60/056,888
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;; EARLIER APPLICATION NUMBER: 60/056,880
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;; EARLIER APPLICATION NUMBER: 60/056,894
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;; EARLIER APPLICATION NUMBER: 60/056,636
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;; EARLIER APPLICATION NUMBER: 60/056,874
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;; EARLIER APPLICATION NUMBER: 60/056,910
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,864
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,631
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,845
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,892
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/057,761
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/047,595

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 2.5%; Score 19; DB 4; Length 1196;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TGATGACGGTGGCTTCACC 387
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Db 134 TGATGACGGTGGCTTCACC 116

RESULT 10
US-09-149-476-57/c
; Sequence 57, Application us/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002p1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
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EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

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Db 128 TGATGACGGTGGCTTCACC 110

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US-09-213-768-1/c
Sequence 1, Application US/09213768
Patent No. 5985664
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
FILE REFERENCE: RTS-0026
CURRENT APPLICATION NUMBER: US/09/213, 768
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1

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; LENGTH: 1514
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(441)
US-09-213-768-1

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; Sequence 13, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_flg-genes Version 2.0
; SEQ ID NO 13
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (130)..(1539)
US-09-668-680-13

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Db      774 CTTCCTGCTGCTTCTCTCA 792

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RESULT 13
US-09-213-768-2/c
; Sequence 2, Application US/09213768
; Patent No. 5985664
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2

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; LENGTH: 20
; TYPE: DNA
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; OTHER INFORMATION: PCR Primer
US-09-213-768-2

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RESULT 14
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; Sequence 1, Application US/08249380
; Patent No. 5827685
; GENERAL INFORMATION:
; APPLICANT: Lindquist, Susan
; TITLE OF INVENTION: Methods and Compositions of Genetic
; TITLE OF INVENTION: Stress Response Systems
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,380
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/710,187
; FILING DATE: 31-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-249-380-1

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-09-182-145-152/c
; Sequence 152, Application US/09182145B
; Patent No. 6387657

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	753	100.0	1708	US-10-010-408-1	Sequence 1, Appli
3	681	90.4	681	US-10-010-408-12	Sequence 12, Appli
4	210	27.9	210	US-10-010-408-8	Sequence 8, Appli
5	177	23.5	177	US-10-010-408-5	Sequence 5, Appli
6	174	23.1	174	US-10-010-408-10	Sequence 10, Appli
7	90	12.0	1734	US-10-112-267-17	Sequence 17, Appli
8	90	12.0	1734	US-10-112-267-18	Sequence 18, Appli
9	32	4.2	199	US-09-864-761-23432	Sequence 23432, A
10	32	4.2	586	US-09-864-761-6698	Sequence 6698, Ap
11	32	4.2	738	US-10-112-267-38	Sequence 38, Appli
12	32	4.2	841	US-10-112-267-39	Sequence 39, Appli
13	32	4.2	1266	US-10-137-866-319	Sequence 319, App
14	32	4.2	1266	US-10-146-726-319	Sequence 319, App
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16	32	4.2	1266	US-10-146-788-319	Sequence 319, App

17	32	4.2	1266	14	US-10-152-380-319	Sequence 319, App
18	32	4.2	1266	14	US-10-153-934-319	Sequence 319, App
19	32	4.2	1266	15	US-10-028-072-319	Sequence 319, App
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25	32	4.2	1266	15	US-10-176-921-319	Sequence 319, App
26	32	4.2	1266	15	US-10-137-865-319	Sequence 319, App
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34	32	4.2	1266	15	US-10-121-050-319	Sequence 319, App
35	32	4.2	1266	15	US-10-141-755-319	Sequence 319, App
36	32	4.2	1266	15	US-10-143-032-319	Sequence 319, App
37	32	4.2	1266	15	US-10-123-108-319	Sequence 319, App
38	32	4.2	1266	15	US-10-123-236-319	Sequence 319, App
39	32	4.2	1266	15	US-10-123-261-319	Sequence 319, App
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44	32	4.2	1266	15	US-10-123-903-319	Sequence 319, App
45	32	4.2	1266	15	US-10-124-819-319	Sequence 319, App

ALIGNMENTS

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US-10-010-408-3
; Sequence 3, Application US/10010408
; Publication No. US20020165185A1

GENERAL INFORMATION:
; APPLICANT: John J. Castellot, Jr.
; TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
; and Uses Therefor

NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,408
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/044,273
; FILING DATE: March 19, 1998
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;

LENGTH: 753 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..750
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-010-408-3

Query Match 100.0%; Score 753; DB 15; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGGGGAGCCCACTGATCATCTTCTGGCCACTTCTCTCTCTCTCTCAATG 60
DB 1 ATGAGGGGAGCCCACTGATCATCTTCTGGCCACTTCTCTCTCTCTCTCAATG 60
OY 61 GTGTGTGCCCCAGCTGTGCGGACACCTGTACCTGTCTTGACACCACTGAGGCTG 120
DB 61 GTGTGTGCCCCAGCTGTGCGGACACCTGTACCTGTCTTGACACCACTGAGGCTG 120
OY 121 CAGGGGTACCCCTGTGCTGATGAGTGGCTGTCTTAAGTGTGTGACAGGAGGCTG 180
DB 121 CAGGGGTACCCCTGTGCTGATGAGTGGCTGTCTTAAGTGTGTGACAGGAGGCTG 180
OY 181 GGGAGTCTCTGCGACCACTGATGTCGACACCCAGAGGCTGTGTTGTCAGCCT 240
DB 181 GGGAGTCTCTGCGACCACTGATGTCGACACCCAGAGGCTGTGTTGTCAGCCT 240
OY 241 GGGGAGGCCCCGTGGCGCATGGGGCTGTGTCTCTTGATGAGATGAGGAGTGTG 300
DB 241 GGGGAGGCCCCGTGGCGCATGGGGCTGTGTCTCTTGATGAGATGAGGAGTGTG 300
OY 301 GAGGTGAATGGCCGAGGTACCTGTGATGAGAGACCTTTAAACCAATTGACGGTCTG 360
DB 301 GAGGTGAATGGCCGAGGTACCTGTGATGAGAGACCTTTAAACCAATTGACGGTCTG 360
OY 361 TGCCGCTGTGATGACGGTGTGCTTACCTGCTGCGCTGTGAGTGAAGTGTGCGGCTG 420
DB 361 TGCCGCTGTGATGACGGTGTGCTTACCTGCTGCGCTGTGAGTGAAGTGTGCGGCTG 420
OY 421 CCCAGCTGGGACTGCCCCAGCCCAAGAAATACAGGTGCAGAAAGTGTGCCCCGAG 480
DB 421 CCCAGCTGGGACTGCCCCAGCCCAAGAAATACAGGTGCAGAAAGTGTGCCCCGAG 480
OY 481 TGGGTATGTAGCAGGAGTGAACACCGGATCCAGCGCTCCACGGCGCAAGACCA 540
DB 481 TGGGTATGTAGCAGGAGTGAACACCGGATCCAGCGCTCCACGGCGCAAGACCA 540
OY 541 CTTTCTGCCCCCTGTCACTCTGCTCTGTGATGCTCTTGTCCAAATTGAGACACAGCC 600
DB 541 CTTTCTGCCCCCTGTCACTCTGCTCTGTGATGCTCTTGTCCAAATTGAGACACAGCC 600
OY 601 TGGGGCCCCCTGCTCAACCACTGTGGGCTGGGATAGCCACCCGAGTGTCCAACAGAAC 660
DB 601 TGGGGCCCCCTGCTCAACCACTGTGGGCTGGGATAGCCACCCGAGTGTCCAACAGAAC 660
OY 661 CGATTCTGCAACTGAGATCCAAAGCGGCTGTGTCTGAGACACCTGCTGAGAGCC 720
DB 661 CGATTCTGCAACTGAGATCCAAAGCGGCTGTGTCTGAGACACCTGCTGAGAGCC 720
OY 721 AGGAGCCACAGCTCATGGAACAGTGTCTTCTAA 753
DB 721 AGGAGCCACAGCTCATGGAACAGTGTCTTCTAA 753

RESULT 2
US-10-010-408-1
; Sequence 1, Application US/10010408
; Publication No. US20020165185A1
; GENERAL INFORMATION:

APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1708 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 249..1001
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-010-408-1
Query Match 100.0%; Score 753; DB 15; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGAGGGGAGCCCACTGATCATCTTCTGGCCACTTCTCTCTCTCTCTCAATG 60
DB 249 ATGAGGGGAGCCCACTGATCATCTTCTGGCCACTTCTCTCTCTCTCTCAATG 308
OY 61 GTGTGTGCCCCAGCTGTGCGGACACCTGTACCTGTCTTGACACCACTGAGGCTG 120
DB 309 GTGTGTGCCCCAGCTGTGCGGACACCTGTACCTGTCTTGACACCACTGAGGCTG 368
OY 121 CAGGGGTACCCCTGTGCTGATGAGTGGCTGTGCTGTAAGTGTGTGACAGGAGGCTG 180
DB 369 CAGGGGTACCCCTGTGCTGATGAGTGGCTGTGCTGTAAGTGTGTGACAGGAGGCTG 428
OY 181 GGGAGTCTCTGCGACCACTGATGTCGACACCCAGAGGCTGTGTTGTCAAGCT 240
DB 429 GGGAGTCTCTGCGACCACTGATGTCGACACCCAGAGGCTGTGTTGTCAAGCT 488
OY 241 GGGGAGGCCCCGTGGCGCATGGGGCTGTGTCTCTTGATGAGATGACGGTGTG 300
DB 489 GGGGAGGCCCCGTGGCGCATGGGGCTGTGTCTCTTGATGAGATGACGGTGTG 548
OY 301 GAGGTGAATGGCCGAGGTACCTGTGATGAGAGACCTTTAAACCAATTGACGGTCTG 360
DB 549 GAGGTGAATGGCCGAGGTACCTGTGATGAGAGACCTTTAAACCAATTGACGGTCTG 608

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QY 361 TGCCGCTGTGATGACGGTGGCTTCACTGCGCTGCGCTGTGACAGTGAGATGTGCGGCTG 420
Db 609 TGCCGCTGTGATGACGGTGGCTTCACTGCGCTGCGCTGTGACAGTGAGATGTGCGGCTG 668
QY 421 CCCAGCTGGAGCTGCCACGCCCAAGAGATACAGGTGCCAGGAAAGTGTGCGCGAG 480
Db 669 CCCAGCTGGAGCTGCCACGCCCAAGAGATACAGGTGCCAGGAAAGTGTGCGCGAG 728
QY 481 TGGGTATGTGACCAAGGAGTACACCGCGATCCAGCGCTCCACGGCGCAAGAGACCA 540
Db 729 TGGGTATGTGACCAAGGAGTACACCGCGATCCAGCGCTCCACGGCGCAAGAGACCA 788
QY 541 CTTTCTGCCCCCTGTGACCTGCTGCTGTGATGCTCCTTGTCCAATTTGAGACAGCC 600
Db 789 CTTTCTGCCCCCTGTGACCTGCTGCTGTGATGCTCCTTGTCCAATTTGAGACAGCC 848
QY 601 TGGGGCCCCCTGTCAACCACTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACCAAG 660
Db 849 TGGGGCCCCCTGTCAACCACTGTGGGCTGGGCATAGCCACCCGAGTGTCCAACCAAG 908
QY 661 CGATTCTGCCAAGTGGAGATCCAAACGCCGCTGTGTCTGCCCCAGAACCCCTGCGCAGCC 720
Db 909 CGATTCTGCCAAGTGGAGATCCAAACGCCGCTGTGTCTGCCCCAGAACCCCTGCGCAGCC 968
QY 721 AGAGCCACAGCTCATGGAACAGTGTCTTCTAA 753
Db 969 AGAGCCACAGCTCATGGAACAGTGTCTTCTAA 1001

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RESULT 3

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US-10-010-408-12
: Sequence 12, Application US/10010408
: Publication No. US20020165185A1
: GENERAL INFORMATION:
: APPLICANT: John J. Castellot, Jr.
: TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
: and Uses Therefor
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/010,408
: FILING DATE: 07-Dec-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/044,273
: FILING DATE: March 19, 1998
: APPLICATION NUMBER: <Unknown>
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Amy E. Mandragouras
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: MBI-004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 681 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA

```

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: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..681
: SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-010-408-12

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```

Query Match 90.4%; Score 681; DB 15; Length 681;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 CAGCTGTGCCGGACACACCTGTACCTGTCTTGGACACACACCCAGTGCCACAGGGGTA 129
Db 1 CAGCTGTGCCGGACACACCTGTACCTGTCTTGGACACACACCCAGTGCCACAGGGGTA 60
QY 130 CCCCCTGGTCTGATGGCTGTGGCTGCTGTAAGTGTGTGACGAGAGGCTGGGGAGTCC 189
Db 61 CCCCCTGGTCTGATGGCTGTGGCTGCTGTAAGTGTGTGACGAGAGGCTGGGGAGTCC 120
QY 190 TGGCAACCACTGCATGTCTGCAACCCCAAGCCAGAGGCGCTGGTTGTCAAGCTGGGGCAGGC 249
Db 121 TGGCAACCACTGCATGTCTGCAACCCCAAGCCAGAGGCGCTGGTTGTCAAGCTGGGGCAGGC 180
QY 250 CCTGGCGGCCATATGGGCTGTGTCTCTTGGATGAGATGACGGTATGAGGTGAT 309
Db 181 CCTGGCGGCCATATGGGCTGTGTCTCTTGGATGAGATGACGGTATGAGGTGAT 240
QY 310 GCGCCAGAGTACCTGATGAGAGACCTTTAAACCAATTCAGAGGTCTGTGCGGCTGT 369
Db 241 GCGCCAGAGTACCTGATGAGAGACCTTTAAACCAATTCAGAGGTCTGTGCGGCTGT 300
QY 370 GATGACGGTGGCTTACCTGCTGCCCTGCGCTGTGACATGAGATGTGGCGCTGCCAGCTGG 429
Db 301 GATGACGGTGGCTTACCTGCTGCCCTGCGCTGTGACATGAGATGTGGCGCTGCCAGCTGG 360
QY 430 GACTGCCCCACGCCCCAAGAGATACAGGTGCCAGGAAAGTGTGCCCCAGTGGTATGT 489
Db 361 GACTGCCCCACGCCCCAAGAGATACAGGTGCCAGGAAAGTGTGCCCCAGTGGTATGT 420
QY 490 GACCAAGGAGTGCACACCGCGGATCCAGCGCTCCACGGCGCAAGACACCACTTTCTGCC 549
Db 421 GACCAAGGAGTGCACACCGCGGATCCAGCGCTCCACGGCGCAAGACACCACTTTCTGCC 480
QY 550 CTTGTCACTCCTGCTCTGTGTGCTCTCTTGTCCAAATTTGAGACACAGCCTGGGGCCCC 609
Db 481 CTTGTCACTCCTGCTCTGTGTGCTCTCTTGTCCAAATTTGAGACACAGCCTGGGGCCCC 540
QY 610 TGCATCAACCACTGTGGGCTGGGCATAGCCACCCAGAGTGTCCAACCAAGACGATTTGC 669
Db 541 TGCATCAACCACTGTGGGCTGGGCATAGCCACCCAGAGTGTCCAACCAAGACGATTTGC 600
QY 670 CAAGTGGAGATCCAAACGCCGCTGTGTCTGCCACAGACCTGCTGGCAGCAGAGCCAC 729
Db 601 CAAGTGGAGATCCAAACGCCGCTGTGTCTGCCACAGACCTGCTGGCAGCAGAGCCAC 660
QY 730 AGCTCATGGAACAGTGTCTTC 750
Db 661 AGCTCATGGAACAGTGTCTTC 681

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RESULT 4

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US-10-010-408-8
: Sequence 8, Application US/10010408
: Publication No. US20020165185A1
: GENERAL INFORMATION:
: APPLICANT: John J. Castellot, Jr.
: TITLE OF INVENTION: No. US20020165185A1e1 Heparin-Induced CCN-Like Molecules
: and Uses Therefor
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts

```


COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..210
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-010-408-8

Query Match 27.9%; Score 210; DB 15; Length 210;
Best Local Similarity 100.0%; Pred. No. 6.4e-99;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CAGCTGTGCGGACACCCCTGTAACCTGTCCTTGACACACCCACCCAGTGCACAGGGGTA 129
|||||
Db 1 CAGCTGTGCGGACACCCCTGTAACCTGTCCTTGACACACCCACCCAGTGCACAGGGGTA 60
QY 130 CCCCTGTGCTGATGGCTGTGCGCTGCTGTAAAGTGTGCGACGAGGCTGGGGAGTCC 189
|||||
Db 61 CCCCTGTGCTGATGGCTGTGCGCTGCTGTAAAGTGTGCGACGAGGCTGGGGAGTCC 120
QY 190 TGGGACCACTGATGTCTGCGACCCAGCCAGGCGCTGTTGTCAAGCTGGGGCAGGC 249
|||||
Db 121 TGGGACCACTGATGTCTGCGACCCAGCCAGGCGCTGTTGTCAAGCTGGGGCAGGC 180
QY 250 CTGGCGGCGCATGGGCTGTGTCTCTTG 279
|||||
Db 181 CTGGCGGCGCATGGGCTGTGTCTCTTG 210

RESULT 5
US-10-010-408-5
Sequence 5, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..177
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-408-5

Query Match 23.5%; Score 177; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGTGAGTGAATGGCCGACGTAACCTGGATGAGAGACCTTTAAACCAATTCAGGCTC 357
|||||
Db 1 TGTGAGTGAATGGCCGACGTAACCTGGATGAGAGACCTTTAAACCAATTCAGGCTC 60
QY 358 CTGTGCGGCTGTGATGACGGGTGCTTCACCTGCCCTGCCCTGTGCAAGTATGTCGG 417
|||||
Db 61 CTGTGCGGCTGTGATGACGGGTGCTTCACCTGCCCTGCCCTGTGCAAGTATGTCGG 120
QY 418 CTGCCAGCTGGGACTGCCACGCCCCCAAGAGAAATACAGGTGCCAGGAAAGTCTGC 474
|||||
Db 121 CTGCCAGCTGGGACTGCCACGCCCCCAAGAGAAATACAGGTGCCAGGAAAGTCTGC 177

RESULT 6
US-10-010-408-10
Sequence 10, Application US/10010408
Publication No. US20020165185A1
GENERAL INFORMATION:
APPLICANT: John J. Castellot, Jr.
TITLE OF INVENTION: No. US20020165185A1 Heparin-Induced CCN-Like Molecules
and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/010,408
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/044,273
FILING DATE: March 19, 1998
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..174
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-408-10

Query Match 23.1%; Score 174; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.3e-80;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 577 CCTGTCCAATTGGAGCAGACCGCTGGGGCCCCCTGCTCAACCACTGTGGGCTGGGCATA 636
|||||
Db 1 CCTGTCCAATTGGAGCAGACCGCTGGGGCCCCCTGCTCAACCACTGTGGGCTGGGCATA 60
QY 637 GCCACCCGAGTGTCCAACGAGACCGATTCTGCCAAGTGAGATCCAGCCGCGCTGTGT 696
|||||
Db 61 GCCACCCGAGTGTCCAACGAGACCGATTCTGCCAAGTGAGATCCAGCCGCGCTGTGT 120
QY 697 CTGCCACAGCCTGCTGGCAGCCAGAGCCACAGCTCATGGAACAGTCTTTC 750
|||||
Db 121 CTGCCACAGCCTGCTGGCAGCCAGAGCCACAGCTCATGGAACAGTCTTTC 174

RESULT 7

US-10-112-267-17

; Sequence 17, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156

; SEQ ID NO 17
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-17

Query Match 12.0%; Score 90; DB 15; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGACGAGAGGCTGGGGAGTCTGCGACCACTGCATGTCTGCGACCCAGCCA 221
|||||
Db 418 AGTGTGACGAGAGGCTGGGGAGTCTGCGACCACTGCATGTCTGCGACCCAGCCA 477
QY 222 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 251
|||||
Db 478 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 507

RESULT 8

US-10-112-267-18/c

; Sequence 18, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 18
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-112-267-18

Query Match 12.0%; Score 90; DB 15; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGACGAGAGGCTGGGGAGTCTGCGACCACTGCATGTCTGCGACCCAGCCA 221
|||||
Db 1317 AGTGTGACGAGAGGCTGGGGAGTCTGCGACCACTGCATGTCTGCGACCCAGCCA 1258
QY 222 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 251
|||||
Db 1257 GGGCCTGTTGTTCAGCCTGGGGCAGGCC 1228

RESULT 9

US-09-864-761-23432

; Sequence 23432, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 23432
LENGTH: 199
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL139352.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: NT HIT: AF083500.1, EVALUATE 1.00e-108
OTHER INFORMATION: SWISSPROT HIT: O19113, EVALUATE 9.00e-19
US-09-864-761-23432
Query Match 4.2%; Score 32; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 406 GAGGATGCGGCTGCCAGCTGGGACTGCC 437
|||||
Db 129 GAGGATGCGGCTGCCAGCTGGGACTGCC 160

RESULT 10

US-09-864-761-6698
Sequence 6698, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6698
LENGTH: 586
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL139352.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
US-09-864-761-6698
Query Match 4.2%; Score 32; DB 10; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 406 GAGGATGCGGCTGCCAGCTGGGACTGCC 437
|||||
Db 129 GAGGATGCGGCTGCCAGCTGGGACTGCC 160

Db 342 GAGGATGTGCGGCTGCCAGCTGGGACTGCC 373

RESULT 11

US-10-112-267-38

; Sequence 38, Application US/10112267

; Publication No. US20030068678A1

; GENERAL INFORMATION:

; APPLICANT: Botstein, David A.

; APPLICANT: Cohen, Robert

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Lawrence, David A.

; APPLICANT: Levine, Arnold J.

; APPLICANT: Pennica, Diane

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: P1176R2

; CURRENT APPLICATION NUMBER: US/10/112,267

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

; NUMBER OF SEQ ID NOS: 156

; SEQ ID NO 38

; LENGTH: 738

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-112-267-38

Query Match 4.2%; Score 32; DB 15; Length 738;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 158

|||||

Db 115 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 146

RESULT 12

US-10-112-267-39

; Sequence 39, Application US/10112267

; Publication No. US20030068678A1

; GENERAL INFORMATION:

; APPLICANT: Botstein, David A.

; APPLICANT: Cohen, Robert

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Lawrence, David A.

; APPLICANT: Levine, Arnold J.

; APPLICANT: Pennica, Diane

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: P1176R2

; CURRENT APPLICATION NUMBER: US/10/112,267

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14

; NUMBER OF SEQ ID NOS: 156

; SEQ ID NO 39

; LENGTH: 841

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1-841

; OTHER INFORMATION: Sequence is synthesized.

US-10-112-267-39

Query Match 4.2%; Score 32; DB 15; Length 841;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGGATGTGCGGCTGCCAGCTGGGACTGCC 437

|||||

Db 417 GAGGATGTGCGGCTGCCAGCTGGGACTGCC 448

RESULT 13

US-10-137-866-319

; Sequence 319, Application US/10137866

; Publication No. US20030129689A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerlitsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C151

; CURRENT APPLICATION NUMBER: US/10/137,866

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059836

; PRIOR FILING DATE: 1997-09-24

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/062285

; PRIOR FILING DATE: 1997-10-17

1	PRIOR APPLICATION NUMBER: 60/062287
2	PRIOR FILING DATE: 1997-10-17
3	PRIOR APPLICATION NUMBER: 60/062814
4	PRIOR FILING DATE: 1997-10-24
5	PRIOR APPLICATION NUMBER: 60/062816
6	PRIOR FILING DATE: 1997-10-24
7	PRIOR APPLICATION NUMBER: 60/063045
8	PRIOR FILING DATE: 1997-10-24
9	PRIOR APPLICATION NUMBER: 60/063082
10	PRIOR FILING DATE: 1997-10-31
11	PRIOR APPLICATION NUMBER: 60/063127
12	PRIOR FILING DATE: 1997-10-24
13	PRIOR APPLICATION NUMBER: 60/063327
14	PRIOR FILING DATE: 1997-10-27
15	PRIOR APPLICATION NUMBER: 60/063329
16	PRIOR FILING DATE: 1997-10-27
17	PRIOR APPLICATION NUMBER: 60/063550
18	PRIOR FILING DATE: 1997-10-28
19	PRIOR APPLICATION NUMBER: 60/063561
20	PRIOR FILING DATE: 1997-10-28
21	PRIOR APPLICATION NUMBER: 60/063704
22	PRIOR FILING DATE: 1997-10-29
23	PRIOR APPLICATION NUMBER: 60/063733
24	PRIOR FILING DATE: 1997-10-29
25	PRIOR APPLICATION NUMBER: 60/063735
26	PRIOR FILING DATE: 1997-10-29
27	PRIOR APPLICATION NUMBER: 60/063738
28	PRIOR FILING DATE: 1997-10-29
29	PRIOR APPLICATION NUMBER: 60/063755
30	PRIOR FILING DATE: 1997-10-17
31	PRIOR APPLICATION NUMBER: 60/064248
32	PRIOR FILING DATE: 1997-11-03
33	PRIOR APPLICATION NUMBER: 60/064809
34	PRIOR FILING DATE: 1997-11-07
35	PRIOR APPLICATION NUMBER: 60/065186
36	PRIOR FILING DATE: 1997-11-12
37	PRIOR APPLICATION NUMBER: 60/065846
38	PRIOR FILING DATE: 1997-11-17
39	PRIOR APPLICATION NUMBER: 60/066364
40	PRIOR FILING DATE: 1997-11-21
41	PRIOR APPLICATION NUMBER: 60/066453
42	PRIOR FILING DATE: 1997-11-24
43	PRIOR APPLICATION NUMBER: 60/066511
44	PRIOR FILING DATE: 1997-11-24
45	PRIOR APPLICATION NUMBER: 60/066770
46	PRIOR FILING DATE: 1997-11-24
47	PRIOR APPLICATION NUMBER: 60/069212
48	PRIOR FILING DATE: 1997-12-11
49	PRIOR APPLICATION NUMBER: 60/069278
50	PRIOR FILING DATE: 1997-12-11
51	PRIOR APPLICATION NUMBER: 60/069334
52	PRIOR FILING DATE: 1997-12-11
53	PRIOR APPLICATION NUMBER: 60/069694
54	PRIOR FILING DATE: 1997-12-16
55	PRIOR APPLICATION NUMBER: 60/072320
56	PRIOR FILING DATE: 1998-01-23
57	PRIOR APPLICATION NUMBER: 60/073612
58	PRIOR FILING DATE: 1998-02-04
59	PRIOR APPLICATION NUMBER: 60/074086
60	PRIOR FILING DATE: 1998-02-09
61	PRIOR APPLICATION NUMBER: 60/074092
62	PRIOR FILING DATE: 1998-02-09
63	PRIOR APPLICATION NUMBER: 60/077791
64	PRIOR FILING DATE: 1998-03-12
65	PRIOR APPLICATION NUMBER: 60/078910
66	PRIOR FILING DATE: 1998-03-20
67	PRIOR APPLICATION NUMBER: 60/079294
68	PRIOR FILING DATE: 1998-03-25
69	PRIOR APPLICATION NUMBER: 60/079663
70	PRIOR FILING DATE: 1998-02-27
71	PRIOR APPLICATION NUMBER: 60/079728
72	PRIOR FILING DATE: 1998-03-27
73	PRIOR APPLICATION NUMBER: 60/080165

1	PRIOR FILING DATE: 1998-03-31
2	PRIOR APPLICATION NUMBER: 60/081203
3	PRIOR FILING DATE: 1998-04-09
4	PRIOR APPLICATION NUMBER: 60/081229
5	PRIOR FILING DATE: 1998-04-09
6	PRIOR APPLICATION NUMBER: 60/081695
7	PRIOR FILING DATE: 1998-04-14
8	PRIOR APPLICATION NUMBER: 60/081817
9	PRIOR FILING DATE: 1998-04-15
10	PRIOR APPLICATION NUMBER: 60/081818
11	PRIOR FILING DATE: 1998-04-15
12	PRIOR APPLICATION NUMBER: 60/082999
13	PRIOR FILING DATE: 1998-04-24
14	PRIOR APPLICATION NUMBER: 60/083322
15	PRIOR FILING DATE: 1998-04-28
16	PRIOR APPLICATION NUMBER: 60/083545
17	PRIOR FILING DATE: 1998-04-29
18	PRIOR APPLICATION NUMBER: 60/084600
19	PRIOR FILING DATE: 1998-05-07
20	PRIOR APPLICATION NUMBER: 60/084627
21	PRIOR FILING DATE: 1998-05-07
22	PRIOR APPLICATION NUMBER: 60/084637
23	PRIOR FILING DATE: 1998-05-07
24	PRIOR APPLICATION NUMBER: 60/085149
25	PRIOR FILING DATE: 1998-05-12
26	PRIOR APPLICATION NUMBER: 60/085323
27	PRIOR FILING DATE: 1998-05-13
28	PRIOR APPLICATION NUMBER: 60/085338
29	PRIOR FILING DATE: 1998-05-13
30	PRIOR APPLICATION NUMBER: 60/085339
31	PRIOR FILING DATE: 1998-05-13
32	PRIOR APPLICATION NUMBER: 60/085579
33	PRIOR FILING DATE: 1998-05-15
34	PRIOR APPLICATION NUMBER: 60/085697
35	PRIOR FILING DATE: 1998-05-15
36	PRIOR APPLICATION NUMBER: 60/085704
37	PRIOR FILING DATE: 1998-05-15
38	PRIOR APPLICATION NUMBER: 60/086414
39	PRIOR FILING DATE: 1998-05-22
40	PRIOR APPLICATION NUMBER: 60/086430
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42	PRIOR APPLICATION NUMBER: 60/087106
43	PRIOR FILING DATE: 1998-05-28
44	PRIOR APPLICATION NUMBER: 60/088026
45	PRIOR FILING DATE: 1998-06-04
46	PRIOR APPLICATION NUMBER: 60/088730
47	PRIOR FILING DATE: 1998-06-10
48	PRIOR APPLICATION NUMBER: 60/088741
49	PRIOR FILING DATE: 1998-06-10
50	PRIOR APPLICATION NUMBER: 60/088810
51	PRIOR FILING DATE: 1998-06-10
52	PRIOR APPLICATION NUMBER: 60/088858
53	PRIOR FILING DATE: 19/98-06-11
54	PRIOR APPLICATION NUMBER: 60/089532
55	PRIOR FILING DATE: 1998-06-17
56	PRIOR APPLICATION NUMBER: 60/089599
57	PRIOR FILING DATE: 1998-06-17
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59	PRIOR FILING DATE: 1998-06-18
60	PRIOR APPLICATION NUMBER: 60/089947
61	PRIOR FILING DATE: 1998-06-19
62	PRIOR APPLICATION NUMBER: 60/090349
63	PRIOR FILING DATE: 1998-06-23
64	PRIOR APPLICATION NUMBER: 60/090429
65	PRIOR FILING DATE: 1998-06-24
66	PRIOR APPLICATION NUMBER: 60/090445
67	PRIOR FILING DATE: 1998-06-24
68	PRIOR APPLICATION NUMBER: 60/090538
69	PRIOR FILING DATE: 1998-06-24
70	PRIOR APPLICATION NUMBER: 60/090863
71	PRIOR FILING DATE: 1998-06-26
72	PRIOR APPLICATION NUMBER: 60/091360
73	PRIOR FILING DATE: 1998-07-01

;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982

Query Match 4.2%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 158
|||
DB 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

RESULT 14
US-10-146-726-319

;; Sequence 319, Application US/10146726
;; Publication No. US20030129690A1
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: DeForge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey J.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3330R1C308
;; CURRENT APPLICATION NUMBER: US/10/146,726
;; CURRENT FILING DATE: 2002-05-15
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 319
;; LENGTH: 1266
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-146-726-319

Query Match 4.2%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 158
|||
DB 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

RESULT 15
US-10-146-727-319

;; Sequence 319, Application US/10146727
;; Publication No. US20030129691A1
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: DeForge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey J.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven

;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3330R1C312
;; CURRENT APPLICATION NUMBER: US/10/146,727
;; CURRENT FILING DATE: 2002-05-15
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 319
;; LENGTH: 1266
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-146-727-319

Query Match 4.2%; Score 32; DB 14; Length 1266;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 158
|||
DB 136 GTACCCCTGCTGCTGATGGCTGTGCTGCTG 167

Search completed: July 28, 2003, 15:36:37
Job time : 185.44 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 15:16:26 ; Search time 1335.79 Seconds
(without alignments)
9129.604 Million cell updates/sec

Title: US-10-010-408-3
Perfect score: 753
Sequence: 1 ATGAGGGGCGACCCACTGAT.....CATGGAACAGTCTTCTTAA 753

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	12.0	940	14	BQ937887
2	67	8.9	537	14	BQ560868
3	49	6.5	424	10	BB849097
4	35	4.6	488	9	AA754979
5	35	4.6	966	12	BF141695
6	32	4.2	380	12	BG900020

7	32	4.2	405	12	BG900069	BG900069 HOA51-1-A
8	32	4.2	489	14	BM751866	BM751866 K-EST0028
9	32	4.2	618	12	BG538695	BG538695 60256932
10	32	4.2	620	13	BG928868	BG928868 HNC57-1-D
11	32	4.2	651	13	BI457141	BI457141 603185392
12	32	4.2	749	9	AL555144	AL555144 AL555144
13	32	4.2	750	13	BM043988	BM043988 603620978
14	32	4.2	790	13	BM046275	BM046275 603626068
15	32	4.2	800	13	BI826781	BI826781 603077268
16	32	4.2	886	13	BI822142	BI822142 603039845
17	32	4.2	888	13	BI825652	BI825652 603072631
18	32	4.2	916	13	BI457367	BI457367 603185689
19	32	4.2	928	13	BI161474	BI161474 602864871
20	32	4.2	933	14	BQ278961	BQ278961 AGENCOURT
21	32	4.2	979	14	BQ279131	BQ279131 AGENCOURT
22	32	4.2	1006	14	BM921531	BM921531 AGENCOURT
23	32	4.2	1022	14	BQ952960	BQ952960 AGENCOURT
24	32	4.2	1058	14	BM805088	BM805088 AGENCOURT
25	32	4.2	1073	14	BQ073722	BQ073722 AGENCOURT
26	32	4.2	1166	13	BM543799	BM543799 AGENCOURT
27	32	4.2	1251	14	BQ961357	BQ961357 AGENCOURT
28	32	4.2	1251	14	BQ195526	BQ195526 UI-R-CN1-
29	24	3.2	426	9	AA717584	AA717584 vt97c08.r
30	23	3.1	436	17	AQ095651	AQ095651 HS_3017_A
31	23	3.1	742	13	BI758148	BI758148 603023866
32	23	3.1	792	13	BI823598	BI823598 603040962
33	21	2.8	495	13	BI204749	BI204749 EST522789
34	21	2.8	529	9	AI897896	AI897896 EST267339
35	21	2.8	561	12	BF051668	BF051668 EST436915
36	21	2.8	563	9	AI897344	AI897344 EST266787
37	21	2.8	609	9	AI485142	AI485142 EST243446
38	21	2.8	620	10	AW223381	AW223381 EST300192
39	20	2.7	188	14	H55466	H55466 CHR220405 C
40	20	2.7	319	13	BM389674	BM389674 UI-R-CN1-
41	20	2.7	334	14	BM698298	BM698298 UI-E-DX0-
42	20	2.7	372	12	BF918366	BF918366 RC3-NT012
43	20	2.7	381	10	BE537338	BE537338 601064521
44	20	2.7	391	14	W80867	W80867 zd83a07.r1
45	20	2.7	401	12	BF849398	BF849398 CM3-EN007

ALIGNMENTS

RESULT 1
BQ937887
LOCUS BQ937887 940 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT 8951807 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6476852 5', mRNA sequence.

ACCESSION BQ937887
VERSION BQ937887
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM14017 row: n column: 21
High quality sequence stop: 543.
Location/Qualifiers
1. .940

FEATURES
source

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6476852"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
BASE COUNT 169 a 277 c 288 g 200 t 6 others
ORIGIN

Query Match 12.0%; Score 90; DB 14; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTGCACGGAGGCTGGGGAGTCTCGACACCATGCTGCGACCCAGCCA 221
|||||
DB 444 AGTGTGTGCACGGAGGCTGGGGAGTCTCGACACCATGCTGCGACCCAGCCA 503

OY 222 GGGCCTGGTTGTTCAGCCTGGGGCAGGCC 251
|||||
DB 504 GGGCCTGGTTGTTCAGCCTGGGGCAGGCC 533

RESULT 2 537 bp mRNA linear EST 20-JUN-2002
B0560868
LOCUS H4067A01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
DEFINITION H4067A01 5', mRNA sequence.
ACCESSION B0560868
VERSION B0560868.1 GI:21461753
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 537)
VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin
P.R., Stagg,C.A., Bassey,U., Alba,K., Hattatani,T., Kargul,G.J.,
Luo,A.G. and Ko,M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set

JOURNAL Unpublished (2002)
COMMENT Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4067 row: A column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 537
POLYA-No.

FEATURES

Source Location/Qualifiers
1..537
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="niaEST:H4067A01-5"
/db_xref="taxon:10090"
/clone="H4067A01"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

BASE COUNT 87 a 162 c 166 g 122 t
ORIGIN

Query Match 8.9%; Score 67; DB 14; Length 537;
Best Local Similarity 100.0%; Pred. No. 3.9e-22;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 AGTGTGTGCACGGAGGCTGGGGAGTCTCGACACCATGCTGCGACCCAGCCA 221
|||||
DB 471 AGTGTGTGCACGGAGGCTGGGGAGTCTCGACACCATGCTGCGACCCAGCCA 530

OY 222 GGGCCTG 228
|||||
DB 531 GGGCCTG 537

RESULT 3 424 bp mRNA linear EST 26-NOV-2001
BB849097
LOCUS BB849097 RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION CDNA clone F930006G02 5', mRNA sequence.
ACCESSION BB849097
VERSION BB849097.1 GI:17090551
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 424)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)

TITLE

JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES Location/Qualifiers
Source
1..424
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930006G02"
/clone_lib="RIKEN full-length enriched, adult inner ear"


```

/tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues ; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"
BASE COUNT      65 a      124 c      132 g      103 t
ORIGIN

Query Match      6.5%; Score 49; DB:10; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.1e-13;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      162 AGTGTGTCACGAGCTGGGGAGTCTCCGACCACTGCATGCTGC 210
Db      373 AGTGTGTCACGAGCTGGGGAGTCTCCGACCACTGCATGCTGC 421

RESULT 4
AA754979      488 bp      mRNA      linear      EST 21-JAN-1998
LOCUS      vu55g08.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
ACCESSION      AA754979
VERSION      AA754979
KEYWORDS      AA754979.1 GI:2802177
SOURCE      EST.
ORGANISM      house mouse.
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 488)
REFERENCE      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
              Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
              Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
              Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
              Waterston,R.
              The Washu-HMI Mouse EST Project
              Unpublished (1996)
              Contact: Marra M/Mouse EST Project
              Washu-HMI Mouse EST Project
              Washington University School of Medicinep
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:642454
              Seq primer: -28m13 rev2 ET from Amersham
              High quality sequence stop: 478.
FEATURES
Source
1..488
/organism="Mus musculus"
/db_xref="C57Bl/6J"
/clone_lib="IMAGE:1195358"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTTACCAATCTGAGTGGAGCGCGCGGAGTGTGTTTGTGTTTGTGTTTGTGTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
```

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constructed and normalized by Bento Soares and M.Fatima
Bonafido."
BASE COUNT      110 a      138 c      130 g      110 t
ORIGIN

Query Match      4.6%; Score 35; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      649 TCCAACGAGAACCGATTCTGCCCACTGGAGATCCA 683
Db      14 TCCAACGAGAACCGATTCTGCCCACTGGAGATCCA 48

RESULT 5
BF141695      966 bp      mRNA      linear      EST 24-OCT-2000
LOCUS      601790752F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021308 5',
DEFINITION      mRNA sequence.
ACCESSION      BF141695
VERSION      BF141695
KEYWORDS      BF141695.1 GI:10980735
SOURCE      EST.
ORGANISM      house mouse.
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 966)
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
              NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabs-remail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1AM9276 row: h column: 13
              High quality sequence stop: 613.
FEATURES
Source
1..966
/organism="Mus musculus"
/db_xref="CZECH II"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4021308"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      227 a      298 c      258 g      183 t
ORIGIN

Query Match      4.6%; Score 35; DB 12; Length 966;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      649 TCCAACGAGAACCGATTCTGCCCACTGGAGATCCA 683
Db      90 TCCAACGAGAACCGATTCTGCCCACTGGAGATCCA 124

RESULT 6
BG900020      380 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HOA48-1-G2.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA
DEFINITION      , mRNA sequence.
ACCESSION      BG900020
```

VERSION BG900020.1 GI:14310269
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 380)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
source
1.380
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 58 a 139 c 118 g 65 t

ORIGIN

Query Match 4.2%; Score 32; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 158
|||||
206 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 237

RESULT 7
LOCUS BG900069 405 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA51-1-A11.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
CDNA, mRNA sequence.
ACCESSION BG900069
VERSION BG900069
KEYWORDS EST.
SOURCE BG900069.1 GI:14310318
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 405)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
source
1.405
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 62 a 140 c 135 g 68 t

ORIGIN

Query Match 4.2%; Score 32; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 158
|||||
Db 202 GTACCCCTGGTGTGATGGCTGTGGCTGCTG 233

RESULT 8
LOCUS BM751866 489 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0028180 S2SNU668s1 Homo sapiens CDNA clone S2SNU668s1-2-D09
5', mRNA sequence.
ACCESSION BM751866
VERSION BM751866
KEYWORDS EST.
SOURCE BM751866.1 GI:19081484
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 489)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: D column: 09
High quality sequence stop: 489.

FEATURES
source
1.489
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S2SNU668s1-2-D09"
/clone_lib="S2SNU668s1"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-668"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was decapped with tobacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dt-selected
mRNA by priming with dt-tailed vector. The dt-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
After analyzing and sequencing about 2,000 ~ 3,000
colonies in original cDNA library, the abundant cDNAs were

selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel.

After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

BASE COUNT 75 a 173 c 159 g 82 t
ORIGIN

Query Match 4.2%; Score 32; DB 14; Length 489;
Best Local Similarity 100.0%; Pred. No. 8.2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGGATGTGGGCTGCCAGCTGGAGCTGCC 437
|||||
Db 139 GAGGATGTGGGCTGCCAGCTGGAGCTGCC 170

RESULT 9
BG538695 618 bp mRNA linear EST 03-APR-2001
DEFINITION 602566932F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691574 5',
mRNA sequence.
ACCESSION BG538695
VERSION BG538695.1 GI:13530928
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 618)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM1510 row: P column: 07
High quality sequence stop: 499.

FEATURES

source

1. 618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4691574"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcctcgcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCAATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCCGAGGCGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT 95 a 194 c 213 g 116 t
ORIGIN

Query Match 4.2%; Score 32; DB 12; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 158
|||||
Db 291 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 322

RESULT 10
BG928868 620 bp mRNA linear EST 06-NOV-2001
LOCUS BG928868
DEFINITION HNC57-1-D9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG928868
VERSION BG928868.1 GI:14323391
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.

FEATURES
source
1. 620
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HNC (Human Normal Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 97 a 218 c 207 g 98 t
ORIGIN

Query Match 4.2%; Score 32; DB 13; Length 620;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 158
|||||
Db 210 GTACCCCTGTGCTGATGGCTGTGGCTGCTG 241

RESULT 11
BI457141 651 bp mRNA linear EST 21-AUG-2001
LOCUS BI457141
DEFINITION 603185392F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258159 5',
mRNA sequence.
ACCESSION BI457141
VERSION BI457141.1 GI:15247797
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 651)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1869 row: 9 column: 24
High quality sequence stop: 651.
Location/Qualifiers

FEATURES
source

1. 651

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258159"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library. 1"

BASE COUNT 91 a 230 c 219 g 111 t
ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 158
|||||
Db 96 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 127

RESULT 12
AL555144

LOCUS AL555144 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODK007Y021 5
DEFINITION prime, mRNA sequence.
ACCESSION AL555144
VERSION AL555144.1 GI:12896595
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 749)

REFERENCE 1 (bases 1 to 749)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source

1. 749

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODK007Y021"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 128 a 252 c 236 g 133 t
ORIGIN

OY 127 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 158
|||||
Db 432 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 463

RESULT 13
BM043988

LOCUS BM043988 750 bp mRNA linear EST 07-NOV-2001
DEFINITION 603620978F1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5446794 5',
mRNA sequence.
ACCESSION BM043988
VERSION BM043988.1 GI:16773255
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 750)

REFERENCE 1 (bases 1 to 750)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1929 row: k column: 19
High quality sequence stop: 714.
Location/Qualifiers

FEATURES
source

1. 750

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5446794"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

BASE COUNT 112 a 267 c 246 g 125 t
ORIGIN

Query Match 4.2%; Score 32; DB 13; Length 750;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 158
|||||
Db 142 GTACCCCTGCTGCTGATGGCTGTGGCTGCTG 173

RESULT 14
BM046275 790 bp mRNA linear EST 07-NOV-2001
LOCUS BM046275

DEFINITION 603626068F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452480 5',
mRNA sequence.
ACCESSION BM046275
VERSION BM046275.1 GI:16775542
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 790)
NIH-MGC <http://mhc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1944 row: h column: 17
High quality sequence stop: 780.
Location/Qualifiers

FEATURES
Source 1..790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5452480"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 121 a 265 c 269 g 135 t
ORIGIN

Query Match 4.2%; Score 32; DB 13; Length 790;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 GAGGATGTCGGCTGCCAGCTGGGACTGCC 437
|||||
DB 265 GAGGATGTCGGCTGCCAGCTGGGACTGCC 296

RESULT 15
BI826781 800 bp mRNA linear EST 04-OCT-2001
LOCUS 603077268F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5169065 5',
DEFINITION mRNA sequence.
ACCESSION BI826781
VERSION BI826781.1 GI:15938331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 800)
NIH-MGC <http://mhc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM11420 row: g column: 18
High quality sequence stop: 788.
Location/Qualifiers

FEATURES
Source 1..800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5169065"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC library."

BASE COUNT 115 a 284 c 264 g 136 t 1 others
ORIGIN

Query Match 4.2%; Score 32; DB 13; Length 800;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GTACCCCTGTGCTGGATGGCTGTGCTGCTG 158
|||||
DB 120 GTACCCCTGTGCTGGATGGCTGTGCTGCTG 151

Search completed: July 28, 2003, 18:02:13
Job time : 1335.79 secs

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